FIGURE 1A

wild type sev-wg sev-wg, lgs^{S17}/+

FIGURE 1B

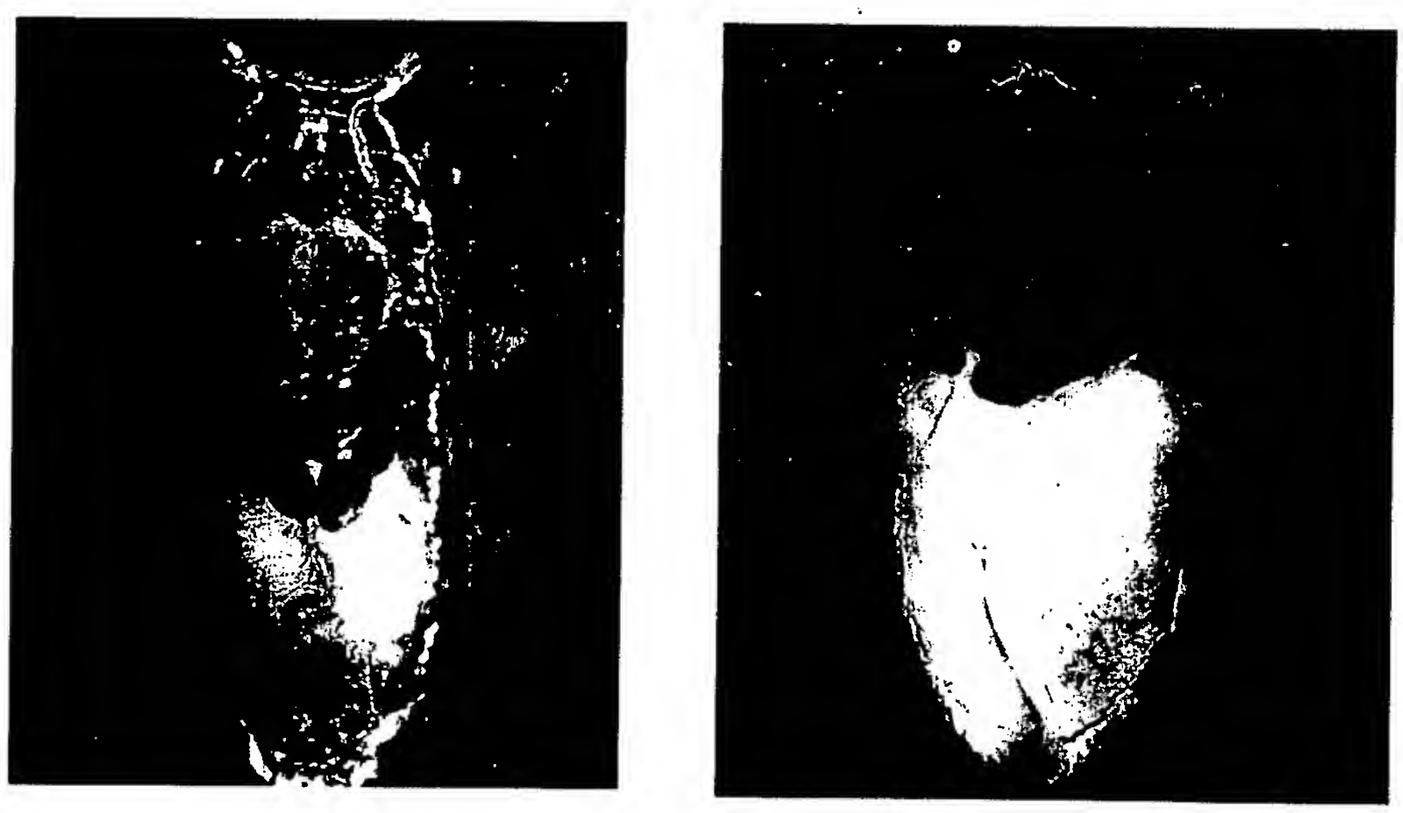

FIGURE 1C

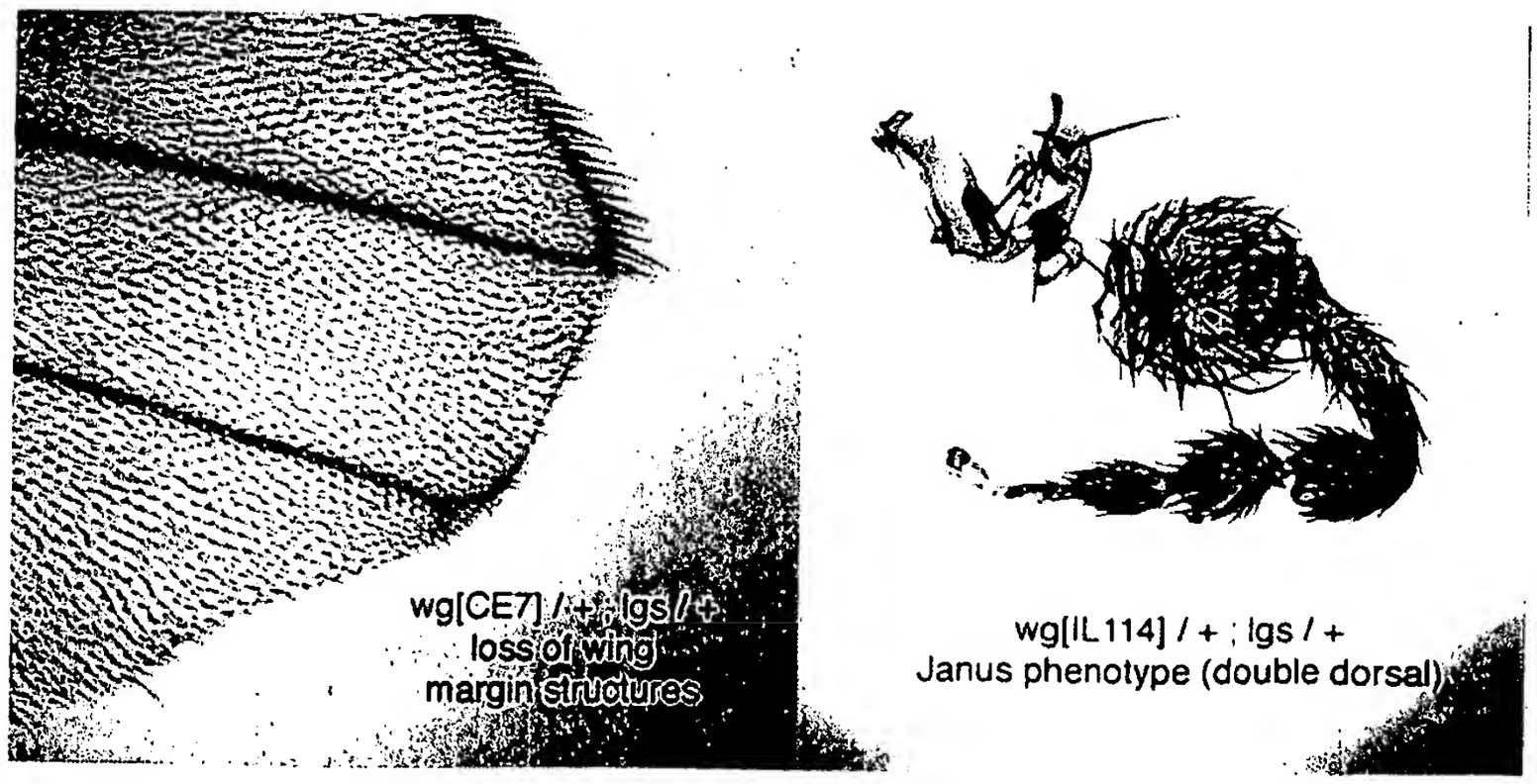

FIGURE 1A

wild type sev-wg sev-wg, lgs^{S17}/+

FIGURE 1B

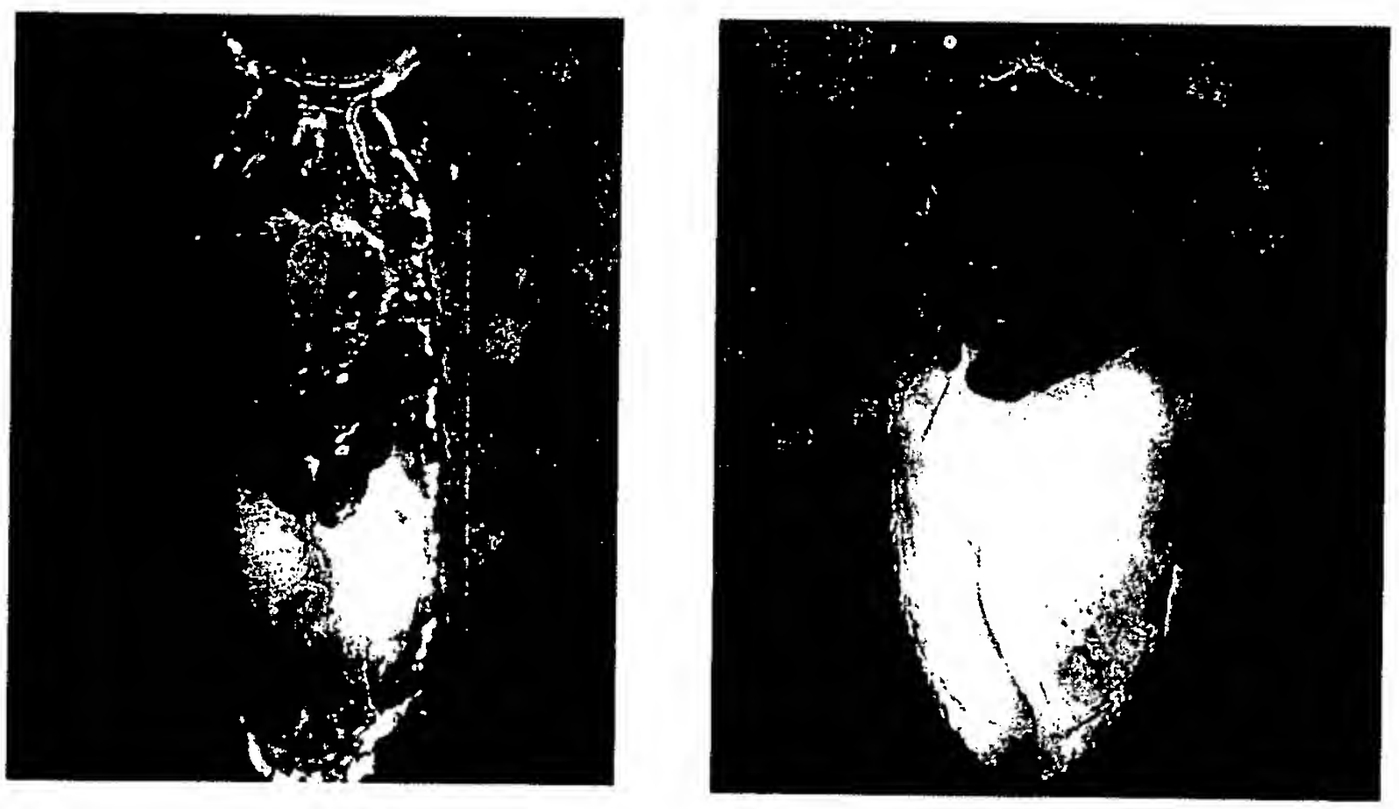

FIGURE 1C

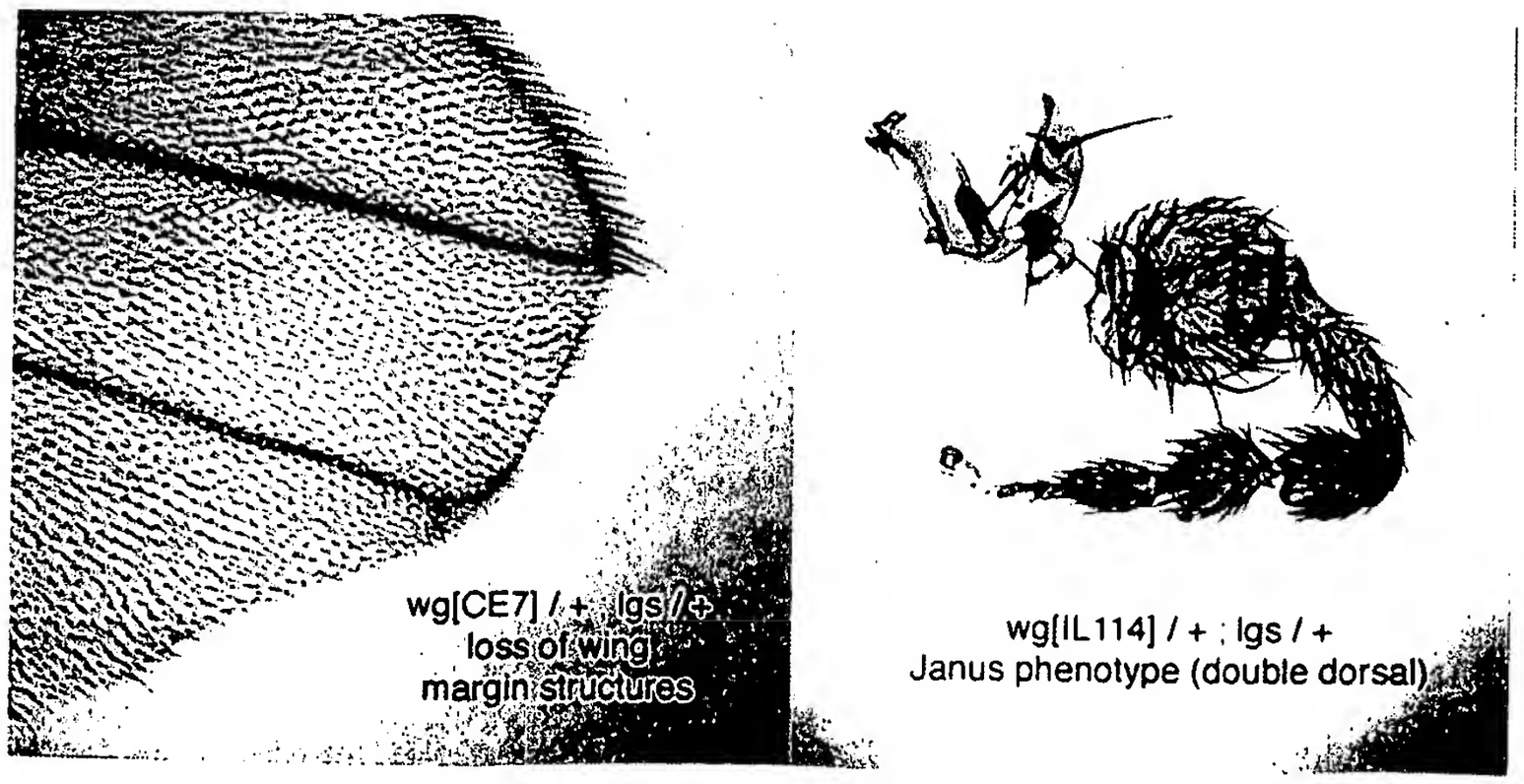

FIGURE 1A

wild type sev-wg sev-wg, lgs^{S17}/+

FIGURE 1B

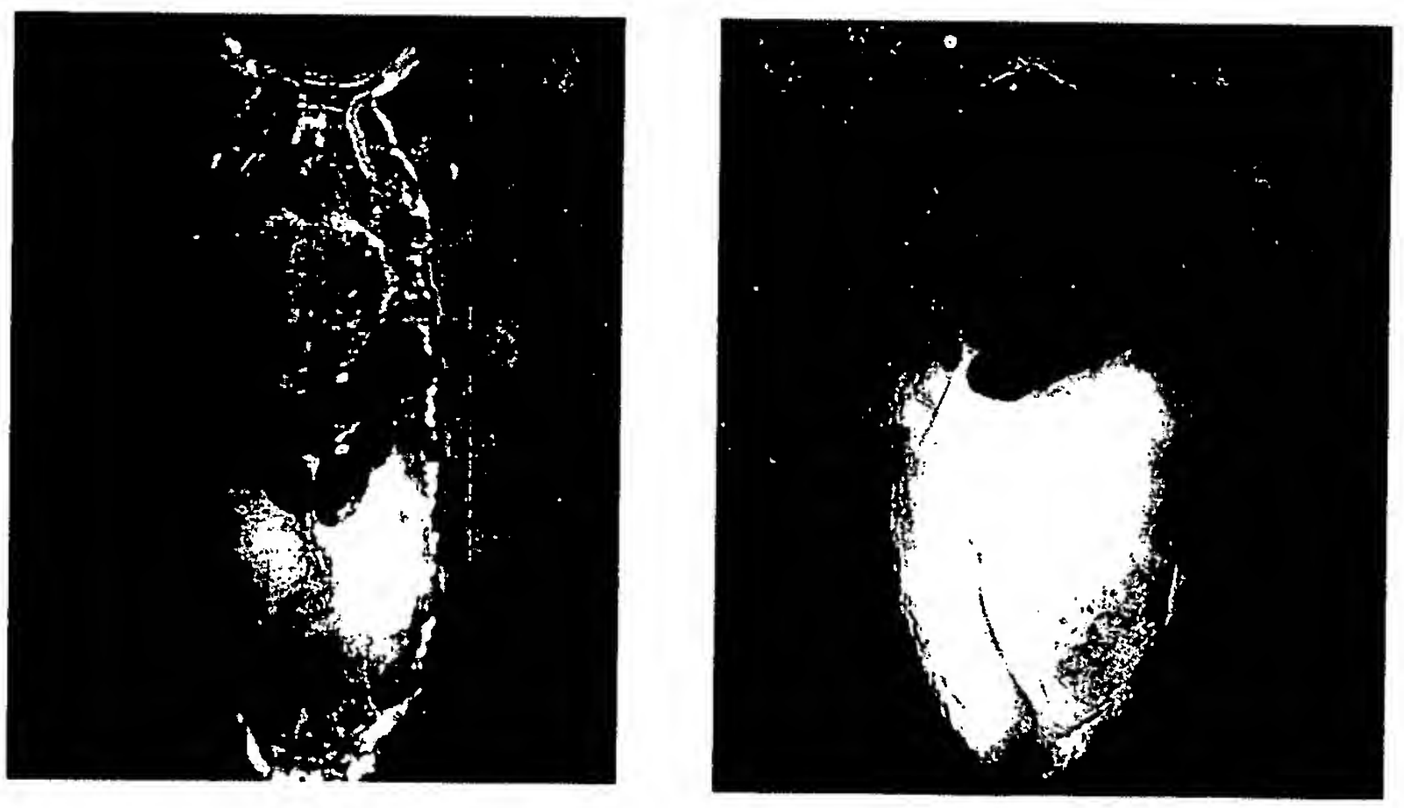

FIGURE 1C

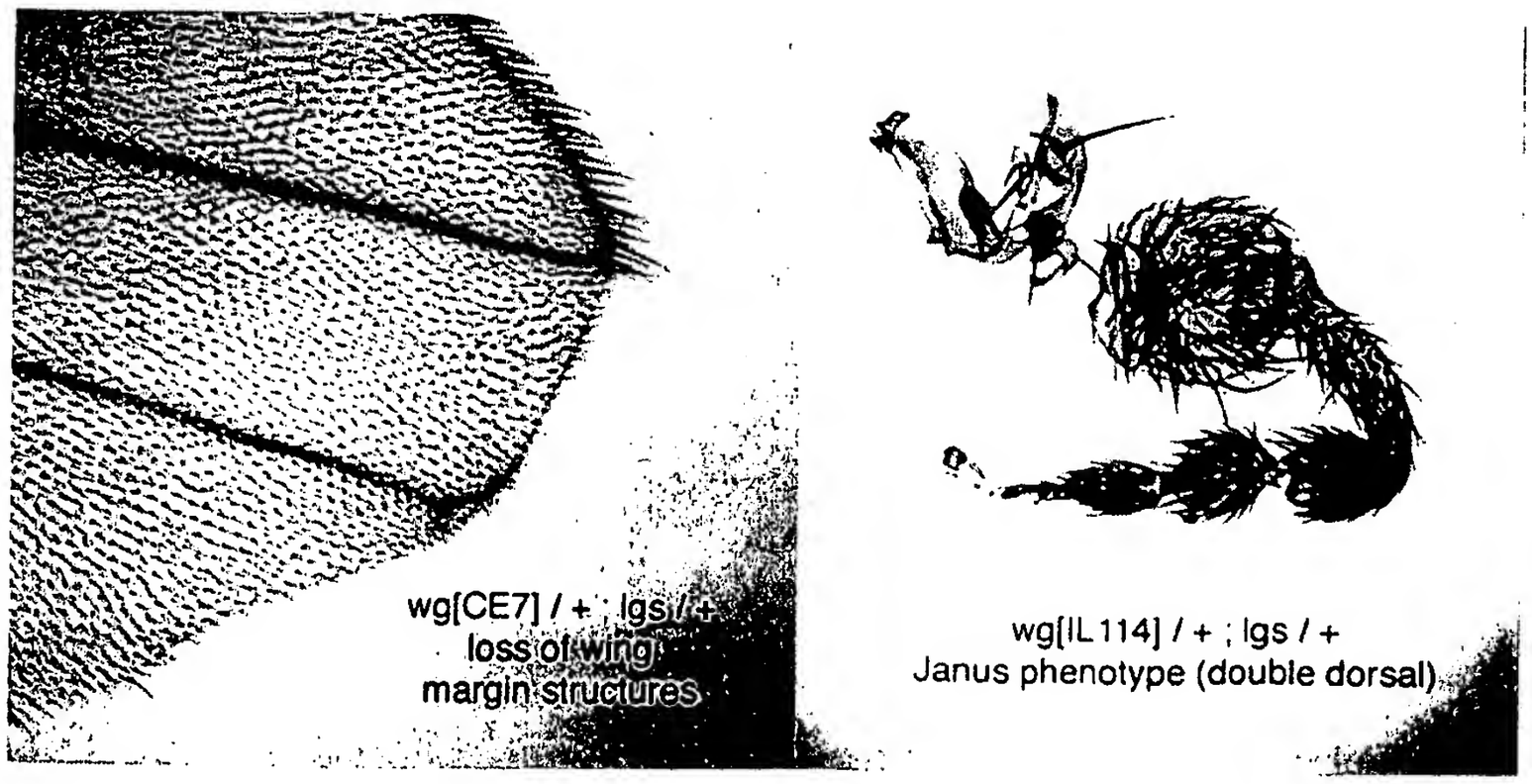

FIG. 2A

```
ACGAGTGCTTCTCTTATTATGCGAGCTGTTTATTCCAAAGTATGTTCGCAATTTTCGACT    60
CCTGCTAACATAACGCACGGTTAAAGCAGGAACATTTGGGCCTATAAGCCCAAAATTTCA   120
TTAGCTTAATACGATGCTCCGAAGTGTTATTGCATTTGCACATATACATAAAATTGTGAC   180
ATAGAATAGGAGAATTCCACATACAAATACAAAAATACAAAATCCTCCAGTAAAATTTAA   240
AACGATATCGTGTTTTGCTTCGCGTATCTCACGTGAGATGTAATCGCATGCATATGAGTG   300
GTGAGTGCCTGCGTGCAGTTCCTGGTCTAAATATGCTTAATTGCGTTCGCCGACTTCAAA   360
AGCAATAAAACGATGGATTTTAATTGCTACTTGAGCAATTAGCCACACAAGGGATCTTGG   420
GAAGGTCGATTTGAAGGAATTCGATTTCTAGGATGCTCTCGACAACAATGCCCCGCAGTC   480
                                              M  P  R  S  P     5

CAACCCAACAACAGCCGCAACCAAACTCCGATGCCTCCTCAACAAGTGCATCTGGATCAA   540
  T  Q  Q  Q  P  Q  P  N  S  D  A  S  S  T  S  A  S  G  S  N    25

ATCCTGGAGCAGCGATCGGAAATGGGGACTCGGCGGCGAGCAGAAGTTCTCCGAAGACCC   600
  P  G  A  A  I  G  N  G  D  S  A  A  S  R  S  S  P  K  T  L    45

TTAATAGCGAACCCTTTTCTACTTTGTCGCCGGGTAAGACTTGTATTGATTTCTCTTTGT   660
  N  S  E  P  F  S  T  L  S  P                                  55

CCGGAATTATAACAACTTTCTGTGTTTCCAGATCAAATAAAATTGACGCCAGAAGAAGGC   720
                                 D  Q  I  K  L  T  P  E  E  G    65

ACTGAGAAAAGCGGACTATCAACTAGTGATAAAGCTGCCACTGGAGGAGCCCCAGGCAGT   780
T  E  K  S  G  L  S  T  S  D  K  A  A  T  G  G  A  P  G  S     85

GGAAATAATCTGCCCGAGGGACAAACTATGCTAAGGCAGAACTCTACGAGCACAATCAAC   840
G  N  N  L  P  E  G  Q  T  M  L  R  Q  N  S  T  S  T  I  N    105

TCGTGCCTAGTCGCTTCTCCACAAAACTCCAGTGAACACTCGAATAGCAGCAATGTGTCT   900
S  C  L  V  A  S  P  Q  N  S  S  E  H  S  N  S  S  N  V  S    125

GCTACAGTGGGCCTTACTCAGATGGTAGATTGTGACGAGCAATCGAAGAAAAACAAATGT   960
A  T  V  G  L  T  Q  M  V  D  C  D  E  Q  S  K  K  N  K  C    145

AGTGTGAAGGACGAGGAAGCTGGTAAGACTGCCCTACAAATGGTTTAAAATTTTAAAATG  1020
S  V  K  D  E  E  A                                           152

TATTGGCGTTCACCTTTGTTAATCATTTAATTGTTTTTTTTTTGCTATACTTACAATTTT  1080

AGTTTTAAACTTGTAAACTTGACTAAAACTCGCGAAGCTCGGATCAAAACAGACATTTTC  1140

TTGGAACCGTAATTAAGCTCATAAAAATATTAATTCATCTTGATGGAATGCATATCATAG  1200
```

FIG. 2B

```
ATGTACTCAAACATCTCAAGAAAGACCTCAAATTGGATCAACTAATTAGTTTGAGAAAAA    1260
ATTGCTGTACTTTTAAGAATATATTAATTTAAAAATTTGCTGAGTGAAATGATATAATAG    1320
TCACAATAATTTTTAGTTAAACTGCTAAAGCATTTTGAATAGCCGTGCTACGCAGATGCT    1380
ACTAGACGCGGTGTAAAAGCTAATTTTTATTTAAAAGCTGTCCTAATATTCCATAACCAT    1440
TAATGTCCCATTTCAGAAATAAGTTCTAATAAAGCAAAAGGTCAAGCAGCTGGTGGCGGC    1500
                E  I  S  S  N  K  A  K  G  Q  A  A  G  G  G      167

TGCGAAACAGGTTCTACATCCAGTTTGACTGTCAAGGAAGAACCCACCGATGTCTTAGGC    1560
C  E  T  G  S  T  S  S  L  T  V  K  E  E  P  T  D  V  L  G      187

AGTTTAGTAAATATGAAAAAAGAAGAAAGAGAAAATCATTCGCCAACGATGTCCCCTGTT    1620
S  L  V  N  M  K  K  E  E  R  E  N  H  S  P  T  M  S  P  V      207

GGTTTTGGTTCAATTGGTAATGCACAGGACAACTCCGCTACACCGGGTAAGTTTTAAGAG    1680
G  F  G  S  I  G  N  A  Q  D  N  S  A  T  P                    222

ATCCATATAAAGCAAATAACAAGAATTAATGTCAGTTACCAATTTTATTTGATAGTCAAA    1740
GAACTACTATAGCGATATCTCCTGCCTTTTAATTTTATTTTAATTAGGAAATACGAATAT    1800
TTCTAATTTGTAAAATAAAATTGATTAATTAACTAGAATTTAAAAACCTTTTGAATTAGG    1860
ACATACCCTTCCAAAAATCAGTAATCATTGGGAACGAGAGTGTGGTCCCGAAGGAGACTA    1920
CTATAAAACCTTTTGAGCTATCTGATACTGCACGCTACTAAAAATGATTAGTTTAGGAAA    1980
ATGGGTGTAATTTTGTAGGAAGTTTTCATTTTAGAAGAAATGTGATTATTTTATTAAACC    2040
CCTTCAAGCGGAACTACATTTGTTCTACGATATTTTGGAAAAACAAATGGTTAAGTTGGA    2100
AAGTGCCTATAAAACAGAATTCCACGGTTTCAAATACTAACCAGGTTTTTGATTTAATTT    2160
TGATTAAATGAGAAATTATCACACTTCAGTTAAAATGTTTAATTCGATTAAGGTCGGACA    2220
ATCACAGCAGATTTCCATTTTTGCGTGTATATATAGAAGTCGCCTTCACACTCTTCTGGC    2280
GCGCTTCACCACTACGTGGAGTTCCGCCCGCAGTGATTTATATAGATGATTTACGAGTTA    2340
TTTAATTTTTTATGGTGTATTTTAATAAATATCTTATTTATTCATTTTACATAGTTAAAA    2400
                                                  V  K  I      225

TTGAAAGAATTTCAAACGACAGTACCACGGAAAAAAAAGGATCGTCCTTGACAATGAATA    2460
  E  R  I  S  N  D  S  T  T  E  K  K  G  S  S  L  T  M  N  N    245

ATGACGAAATGAGCATGGAAGGCTGCAATCAGTTGAATCCCGATTTTATCAATGAATCTT    2520
  D  E  M  S  M  E  G  C  N  Q  L  N  P  D  F  I  N  E  S  L    265
```

FIG. 2C

```
TAAATAATCCTGCAATTTCGAGCATATTAGTAAGCGGAGTAGGACCAATACCCGGAATCG   2580
  N  N  P  A  I  S  S  I  L  V  S  G  V  G  P  I  P  G  I  G   285

GAGTTGGAGCGGGGACGGGAAATTTATTGACTGCCAACGCCAATGGAATCTCCTCGGGTA   2640
  V  G  A  G  T  G  N  L  L  T  A  N  A  N  G  I  S  S  G  S   305

GCAGTAATTGTTTGGATTACATGCAACAGCAAAATCACATATTCGTGTTTTCAACTCAGC   2700
  S  N  C  L  D  Y  M  Q  Q  Q  N  H  I  F  V  F  S  T  Q  L   325

TGGCCAACAAAGGGGCCGAATCAGTTTTAAGCGGTCAATTTCAAACTATTATTGCGTATC   2760
  A  N  K  G  A  E  S  V  L  S  G  Q  F  Q  T  I  I  A  Y  H   345

ACTGCACTCAGCCTGCTACAAAAAGCTTCCTGGAAGACTTTTTTATGAAAAACCCTTTAA   2820
  C  T  Q  P  A  T  K  S  F  L  E  D  F  F  M  K  N  P  L  K   365

AGATTAACAAGTTACAGCGGCACAATTCCGTCGGTATGCCATGGATAGGCATGGGGCAGG   2880
  I  N  K  L  Q  R  H  N  S  V  G  M  P  W  I  G  M  G  Q  V   385

TTGGACTAACTCCTCCTAATCCTGTAGCCAAAATAACACAACAGCAGCCACATACAAAGA   2940
  G  L  T  P  P  N  P  V  A  K  I  T  Q  Q  Q  P  H  T  K  T   405

CCGTAGGCCTATTGAAACCCCAATTCAATCAACATGAAAACAGCAAACGTAGTACTGTAA   3000
  V  G  L  L  K  P  Q  F  N  Q  H  E  N  S  K  R  S  T  V  S   425

GCGCGCCTAGCAACTCTTTTGTCGACCAGTCTGATCCTATGGGCAACGAAACTGAATTGA   3060
  A  P  S  N  S  F  V  D  Q  S  D  P  M  G  N  E  T  E  L  M   445

TGTGCTGGGAAGGCGGATCCTCAAACACCAGTAGGTCTGGACAAAACTCACGAAATCATG   3120
  C  W  E  G  G  S  S  N  T  S  R  S  G  Q  N  S  R  N  H  V   465

TAGACAGTATCAGTACATCCAGCGAGTCACAGGCAATAAAGATACTGGAAGCAGCTGGCG   3180
  D  S  I  S  T  S  S  E  S  Q  A  I  K  I  L  E  A  A  G  V   485

TTGATTTGGGACAGGTCACAAAAGGAAGCGATCCTGGCCTGACAACTGAAAACAACATTG   3240
  D  L  G  Q  V  T  K  G  S  D  P  G  L  T  T  E  N  N  I  V   505

TATCACTGCAAGGAGTTAAGGTTCCAGACGAAAACCTTACACCACAACAGCGGCAACATC   3300
  S  L  Q  G  V  K  V  P  D  E  N  L  T  P  Q  Q  R  Q  H  R   525

GGGAAGAACAGTTGGCAAAAATAAAAAAAAATGAATCAATTTCTTTTTCCTGAAAATGAGA   3360
  E  E  Q  L  A  K  I  K  K  M  N  Q  F  L  F  P  E  N  E  N   545

ATTCAGTAGGAGCTAATGTAAGCTCACAGATAACAAAAATTCCAGGAGATTTAATGATGG   3420
  S  V  G  A  N  V  S  S  Q  I  T  K  I  P  G  D  L  M  M  G   565

GGATGTCGGGTGGCGGAGGCGGATCTATTATAAATCCGACGATGCGACAACTGCATATGC   3480
  M  S  G  G  G  G  G  S  I  I  N  P  T  M  R  Q  L  H  M  P   585

CAGGTAACGCCAAATCGGAGCTCTTATCGGCGACAAGTTCAGGACTTTCGGAAGATGTAA   3540
  G  N  A  K  S  E  L  L  S  A  T  S  S  G  L  S  E  D  V  M   605
```

FIG. 2D

```
TGCATCCAGGGGATGTTATATCAGATATGGGTGCCGTAATAGGATGTAATAATAATCAAA   3600
  H  P  G  D  V  I  S  D  M  G  A  V  I  G  C  N  N  N  Q  K   625

AAACCAGTGTGCAATGTGGATCTGGAGTAGGTGTTGTCACTGGAACAACTGCAGCTGGAG   3660
  T  S  V  Q  C  G  S  G  V  G  V  V  T  G  T  T  A  A  G  V   645

TAAATGTCAATATGCATTGCTCAAGCTCCGGCGCCCCGAATGGCAATATGATGGGAAGCT   3720
  N  V  N  M  H  C  S  S  S  G  A  P  N  G  N  M  M  G  S  S   665

CTACGGATATGCTAGCCTCGTTTGGCAACACAAGCTGCAACGTCATCGGAACGGCCCCAG   3780
  T  D  M  L  A  S  F  G  N  T  S  C  N  V  I  G  T  A  P  D   685

ATATGTCTAAGGAAGTTTTAAATCAAGATAGCCGAACCCATTCACATCAAGGGGGAGTTG   3840
  M  S  K  E  V  L  N  Q  D  S  R  T  H  S  H  Q  G  G  V  A   705

CTCAAATGGAGTGGTCGAAGATTCAACATCAATTTTTCGAAGAACGCCTCAAGGGGGGCA   3900
  Q  M  E  W  S  K  I  Q  H  Q  F  F  E  E  R  L  K  G  G  K   725

AGCCCAGACAAGTCACTGGAACTGTAGTACCACAACAGCAAACCCCTTCTGGATCTGGTG   3960
  P  R  Q  V  T  G  T  V  V  P  Q  Q  Q  T  P  S  G  S  G  G   745

GAAACTCGTTAAACAACCAGGTGCGACCCCTGCAAGGTCCACCTCCTCCTTACCACTCCA   4020
  N  S  L  N  N  Q  V  R  P  L  Q  G  P  P  P  P  Y  H  S  I   765

TCCAGAGATCTGCGTCAGTACCAATAGCCACTCAATCGCCCAATCCCTCGAGTCCAAACA   4080
  Q  R  S  A  S  V  P  I  A  T  Q  S  P  N  P  S  S  P  N  N   785

ATCTATCTCTCCCGTCACCGCGGACAACCGCAGCAGTCATGGGATTGCCGACCAACTCTC   4140
  L  S  L  P  S  P  R  T  T  A  A  V  M  G  L  P  T  N  S  P   805

CTAGCATGGATGGAACAGGATCATTATCTGGATCTGTTCCGCAAGCTAATACTTCGACGG   4200
  S  M  D  G  T  G  S  L  S  G  S  V  P  Q  A  N  T  S  T  V   825

TTCAGGCAGGCACAACAACAGTGCTCTCAGCAAACAAGAACTGTTTTCAGGCAGACACCC   4260
  Q  A  G  T  T  T  V  L  S  A  N  K  N  C  F  Q  A  D  T  P   845

CATCGCCGTCAAATCAAAATCGTAGTAGAAATACCGGATCGTCAAGCGTTCTTACGCATA   4320
  S  P  S  N  Q  N  R  S  R  N  T  G  S  S  S  V  L  T  H  N   865

ACTTAAGCAGCAACCCAAGTACCCCCTTATCTCATCTATCCCCAAAGGAATTTGAGTCTT   4380
  L  S  S  N  P  S  T  P  L  S  H  L  S  P  K  E  F  E  S  F   885

TCGGTCAGTCCTCTGCTGGTATGTTATATTTGTTTAATTTTTTTAAAGACAAATCAAATA   4440
  G  Q  S  S  A                                                890

TGAATTGCGTTAATAATAAGTTATATATTACATAACTCGGAAATTTGATAGAAAAAATCA   4500

GGAATAGAAAAAATAAATTATTTTCCGGACCGCCCATCCATTTCTTGAATCCAATTTCTG   4560

GAGTGATTGTTAGAGATAATCTACTATTAAAATTAAACACGAAAATTCATATCCGTTAAT   4620
```

FIG. 2E

```
TGAAAATCACTATTGTTTAATAAGAAATTAAAAATATGTTTATTATAATATTTCTACAGG    4680
                                                          G     891

TGATAACATGAAAAGTAGGCGACCAAGCCCACAGGGTCAGCGGTCACCAGTAAATAGTCT    4740
 D  N  M  K  S  R  R  P  S  P  Q  G  Q  R  S  P  V  N  S  L     911

AATAGAGGCAAATAAAGATGTACGATTTGCTGCATCCAGTCCTGGTTTTAACCCGCATCC    4800
 I  E  A  N  K  D  V  R  F  A  A  S  S  P  G  F  N  P  H  P     931

ACATATGCAAAGCAATTCAAATTCAGCATTAAACGCCTATAAAATGGGCTCTACCAATAT    4860
 H  M  Q  S  N  S  N  S  A  L  N  A  Y  K  M  G  S  T  N  I     951

ACAGATGGAGGTAAATATTTAAATATTTTATTTAACGTTTTTGTGTTAATTTATCTTCTT    4920
 Q  M  E                                                        954

TTTCAGCGTCAAGCATCAGCGCAAGGTGGATCCGTACAATTTAGTCGGCGCTCCGATAAT    4980
       R  Q  A  S  A  Q  G  G  S  V  Q  F  S  R  R  S  D  N     972

ATTCCGCTAAATCCCAATAGTGGCAATCGGCCGCCACCAAACAAGATGACCCAAAACTTC    5040
I  P  L  N  P  N  S  G  N  R  P  P  P  N  K  M  T  Q  N  F     992

GATCCAATCTCTTCTTTGGCACAAATGTCCCAACAACTAACAAGTTGCGTGTCCAGCATG    5100
D  P  I  S  S  L  A  Q  M  S  Q  Q  L  T  S  C  V  S  S  M    1012

GGTAGTCCAGCCGGAACTGGTGGTATGACGATGATGGGGGGTCCGGGACCGTCCGACATC    5160
```

FIG. 2F

legless

```
G  S  P  A  G  T  G  G  M  T  M  M  G  G  P  G  P  S  D  I      1032
AATATTGAGCATGGAATAATTTCGGGACTAGATGGATCAGGAATAGATACCATAAATCAA   5220
N  I  E  H  G  I  I  S  G  L  D  G  S  G  I  D  T  I  N  Q      1052
AATAACTGTCATTCAATGAATGTCGTAATGAACTCAATGGGTCCCCGAATGCTGAATCCT   5280
N  N  C  H  S  M  N  V  V  M  N  S  M  G  P  R  M  L  N  P      1072
AAAATGTGCGTAGCAGGCGGTCCAAATGGACCGCCTGGCTTTAATCCTAATTCCCCCAAT   5340
K  M  C  V  A  G  G  P  N  G  P  P  G  F  N  P  N  S  P  N      1092
GGTGGATTAAGAGAGAATTCCATAGGGTCTGGCTGTGGCTCAGCAAACTCTTCAAACTTT   5400
G  G  L  R  E  N  S  I  G  S  G  C  G  S  A  N  S  S  N  F      1112
CAAGGGGTTGTTCCACCTGGTGCCAGAATGATGGGTCGAATGCCAGTCAATTTTGGTTCG   5460
Q  G  V  V  P  P  G  A  R  M  M  G  R  M  P  V  N  F  G  S      1132
AATTTCAATCCGAATATTCAGGTAAAGGCGAGTACCCCAAACACCATACAATACATGCCA   5520
N  F  N  P  N  I  Q  V  K  A  S  T  P  N  T  I  Q  Y  M  P      1152
GTAAGGGCACAGAACGCCAACAACAATAACAACAATGGAGCTAATAATGTGCGAATGCCA   5580
V  R  A  Q  N  A  N  N  N  N  N  N  G  A  N  N  V  R  M  P      1172
CCTAGTCTGGAATTTTTGCAGAGGTACGCTAACCCTCAAATGGGTGCTGTAGGCAATGGG   5640
P  S  L  E  F  L  Q  R  Y  A  N  P  Q  M  G  A  V  G  N  G      1192
TCGCCAATATGCCCACCATCAGCCAGCGACGGTACTCCTGGAATGCCAGGATTGATGGCG   5700
S  P  I  C  P  P  S  A  S  D  G  T  P  G  M  P  G  L  M  A      1212
GGACCAGGAGCCGGAGGTATGCTAATGAATTCTTCCGGAGAGCAACACCAGAACAAGATC   5760
G  P  G  A  G  G  M  L  M  N  S  S  G  E  Q  H  Q  N  K  I      1232
ACAAACAATCCTGGGGCAAGCAATGGTATTAACTTCTTTCAGAATTGCAATCAAATGTCT   5820
T  N  N  P  G  A  S  N  G  I  N  F  F  Q  N  C  N  Q  M  S      1252
ATTGTTGACGAAGAGGGTGGATTACCCGGCCATGACGGATCAATGAATATTGGTCAACCA   5880
I  V  D  E  E  G  G  L  P  G  H  D  G  S  M  N  I  G  Q  P      1272
TCTATGATAAGGGGCATGCGTCCACATGCCATGCGGCCAAATGTAATGGGTGCGCGGATG   5940
S  M  I  R  G  M  R  P  H  A  M  R  P  N  V  M  G  A  R  M      1292
CCACCCGTTAACAGGCAAATTCAGTTTGCACAGTCATCGGATGGTATTGACTGTGTCGGG   6000
P  P  V  N  R  Q  I  Q  F  A  Q  S  S  D  G  I  D  C  V  G      1312
GATCCGTCATCATTTTTCACTAACGCTTCCTGCAACAGCGCTGGACCACACATGTTTGGA   6060
D  P  S  S  F  F  T  N  A  S  C  N  S  A  G  P  H  M  F  G      1332
TCAGCACAACAGGCCAATCAGCCTAAGACACAACACATAAAGAACATACCTAGTGGAATG   6120
S  A  Q  Q  A  N  Q  P  K  T  Q  H  I  K  N  I  P  S  G  M      1352
```

FIG. 2G

```
TGTCAAAACCAATCGGGACTTGCAGTGGCACAAGGGCAGATCCAACTGCATGGGCAAGGA   6180
C  Q  N  Q  S  G  L  A  V  A  Q  G  Q  I  Q  L  H  G  Q  G      1372

CATGCGCAGGGTCAGTCTTTAATTGGACCTACTAATAATAATTTAATGTCAACTGCCGGA   6240
H  A  Q  G  Q  S  L  I  G  P  T  N  N  N  L  M  S  T  A  G      1392

AGTGTCAGTGCTACTAACGGTGTCTCTGGCATCAATTTCGTAGGTCCCTCTTCTACGGAC   6300
S  V  S  A  T  N  G  V  S  G  I  N  F  V  G  P  S  S  T  D      1412

CTGAAGTATGCCCAGCAATATCATAGTTTTCAGCAGCAGTTATATGCTACCAACACCAGA   6360
L  K  Y  A  Q  Q  Y  H  S  F  Q  Q  Q  L  Y  A  T  N  T  R      1432

AGTCAACAACAACAGCATATGCACCAGCAGCACCAGAGCAACATGATAACAATGCCGCCG   6420
S  Q  Q  Q  Q  H  M  H  Q  Q  H  Q  S  N  M  I  T  M  P  P      1452

AATTTATCACCAAATCCAACGTTCTTTGTCAACAAATAAACTTCTAAATTTTTGCCGCCC   6480
N  L  S  P  N  P  T  F  F  V  N  K  *                          1465

TCGTCATGTATTGTTTACTAGTCTCCAAATTAAGACATGCATCTCTAAATAAGATTTTTT   6540

GAAGCTTATTTACTTAGGTGTTTTTACAACGGAGAAAATAAACTTTTGGATATGCAAATG   6600

ATAACGTTGGAAACAACATAATTCATTTGCAACTTTTAGAAGTCACGTCGAAGTTAAATG   6660

TAGAATCTGTATTTTAACATAATAGGTCATCTGTAAAAATAATTAAACATCGAAATTTTA   6720

GTTATCAGCAGCTATTTTCTGTTATTATTTAATATGTGCGCTGCTCTCTCTGTGTTAAAT   6780

GAAATTAAAATATATATATAAATGTAAAACGCTATTGATATATATTGCTCTCAACTGTAT   6840

TGTAATCAATATTAAGAGAACTGTAAATTCTTCCATATAAAGGTAATGAAAAAAAAAAAA   6900

AAAAAAAAA                                                       6909
```

FIG. 3A

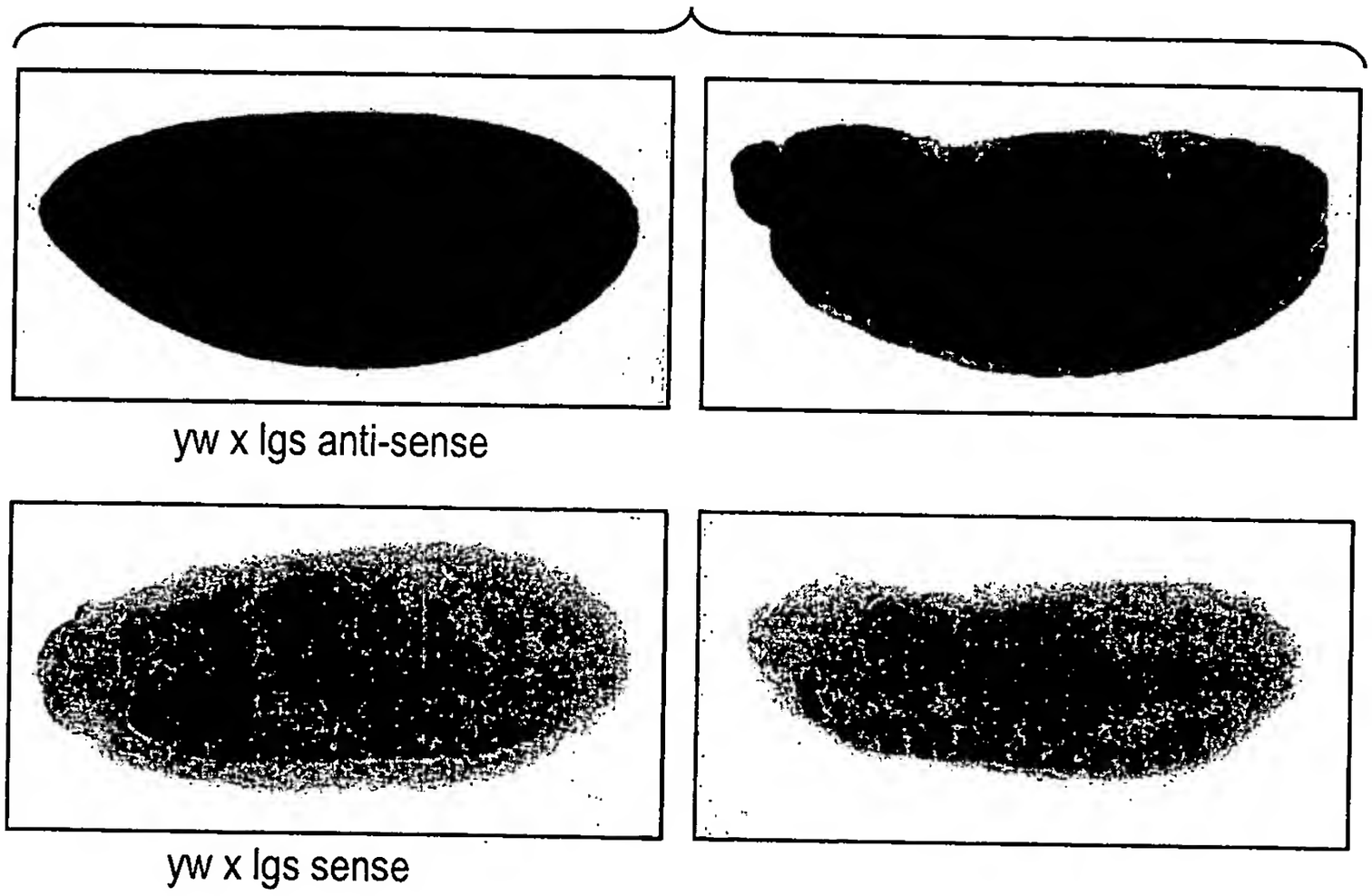

FIG. 3B

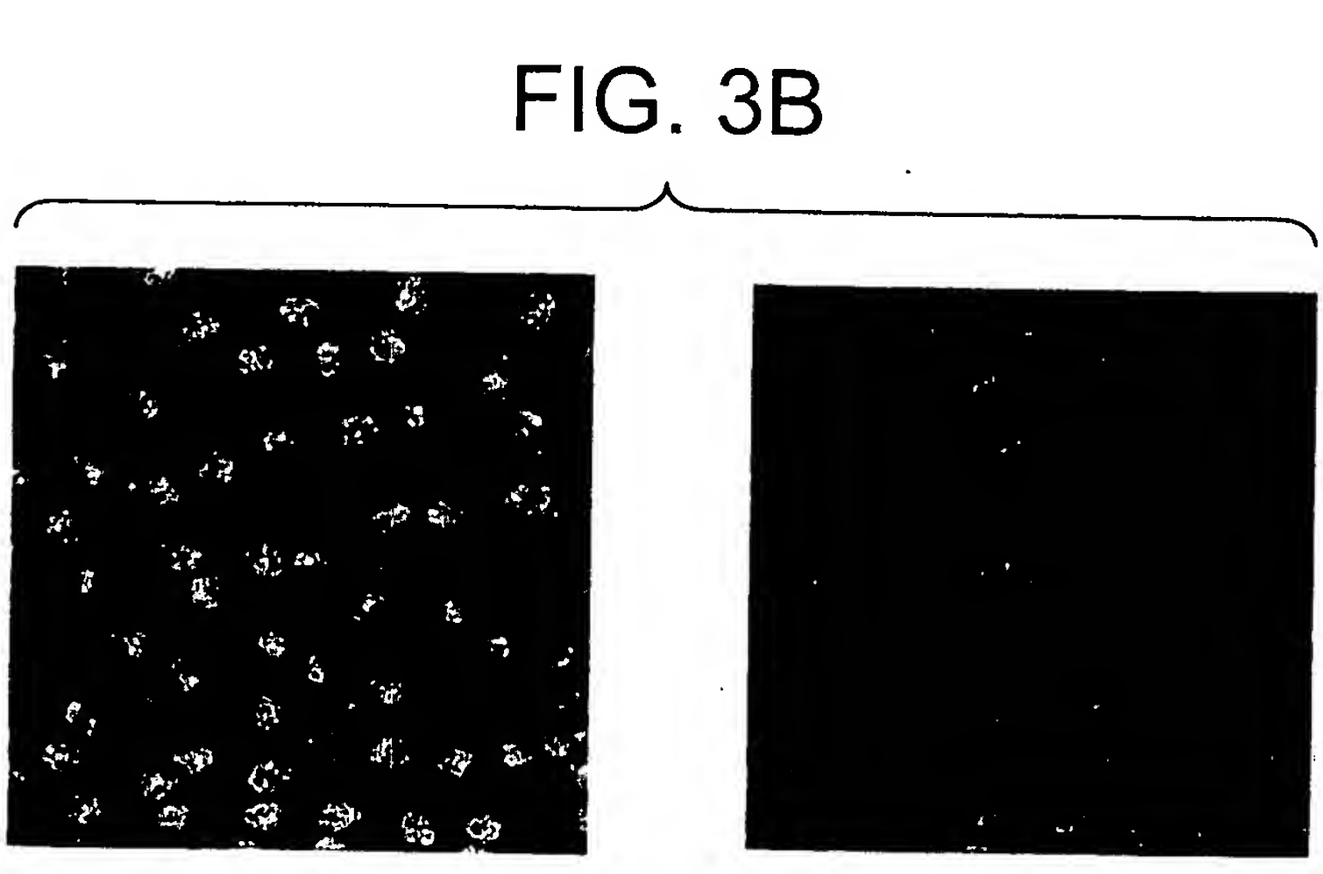

FIG. 4

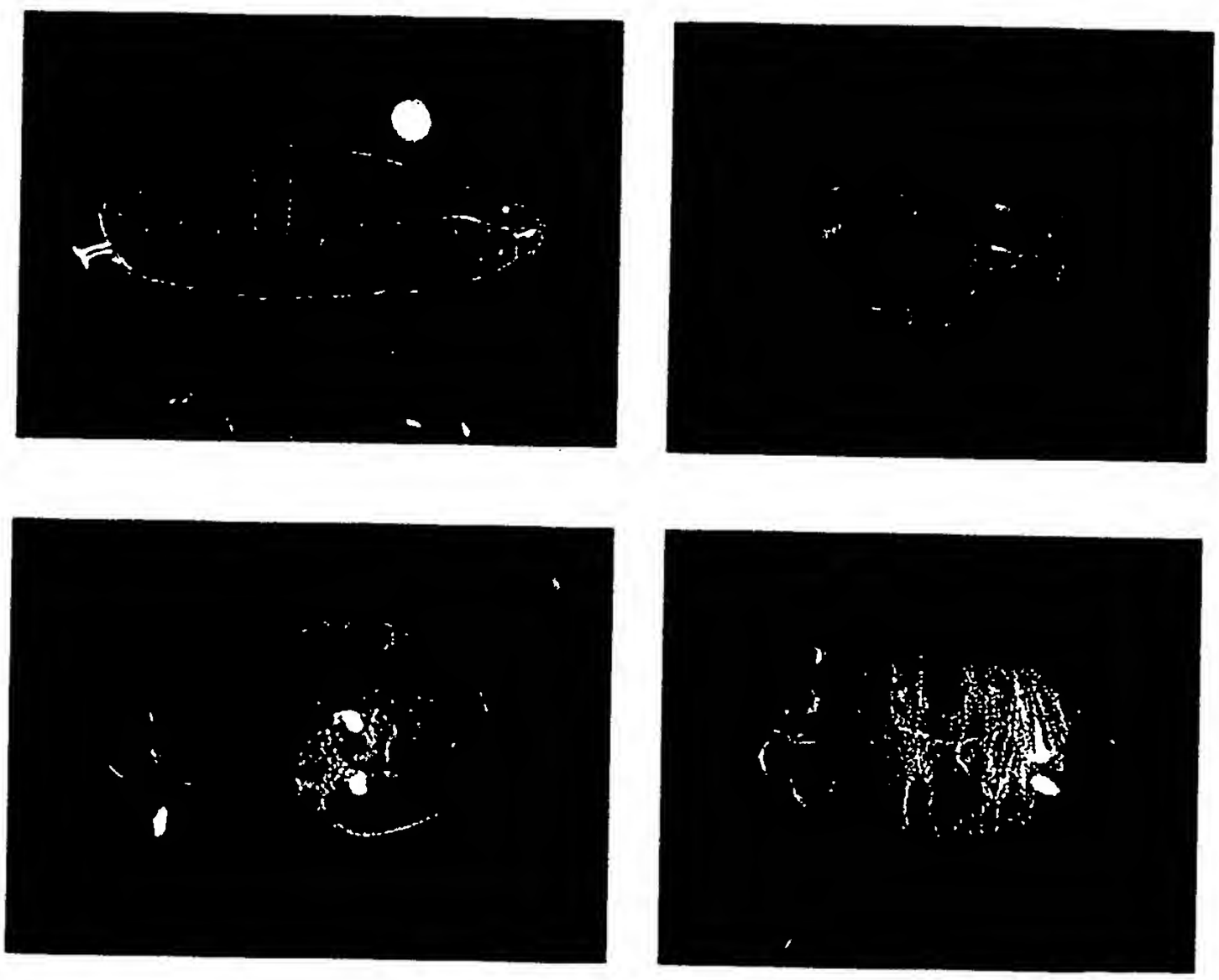

Figure 5A

EGFP-Lgs

Figure 5B

EGFP-Lgs + pcDNA3-Arm-NLS

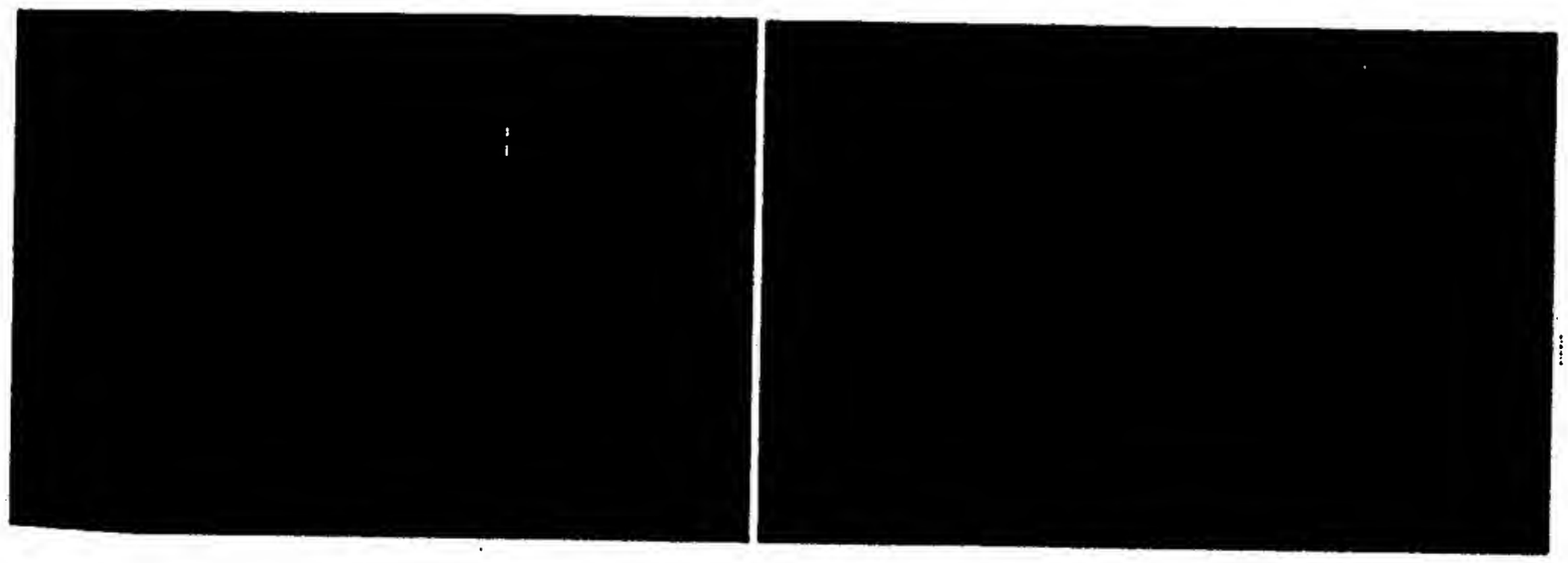

Figure 5A

EGFP-Lgs

Figure 5B

EGFP-Lgs + pcDNA3-Arm-NLS

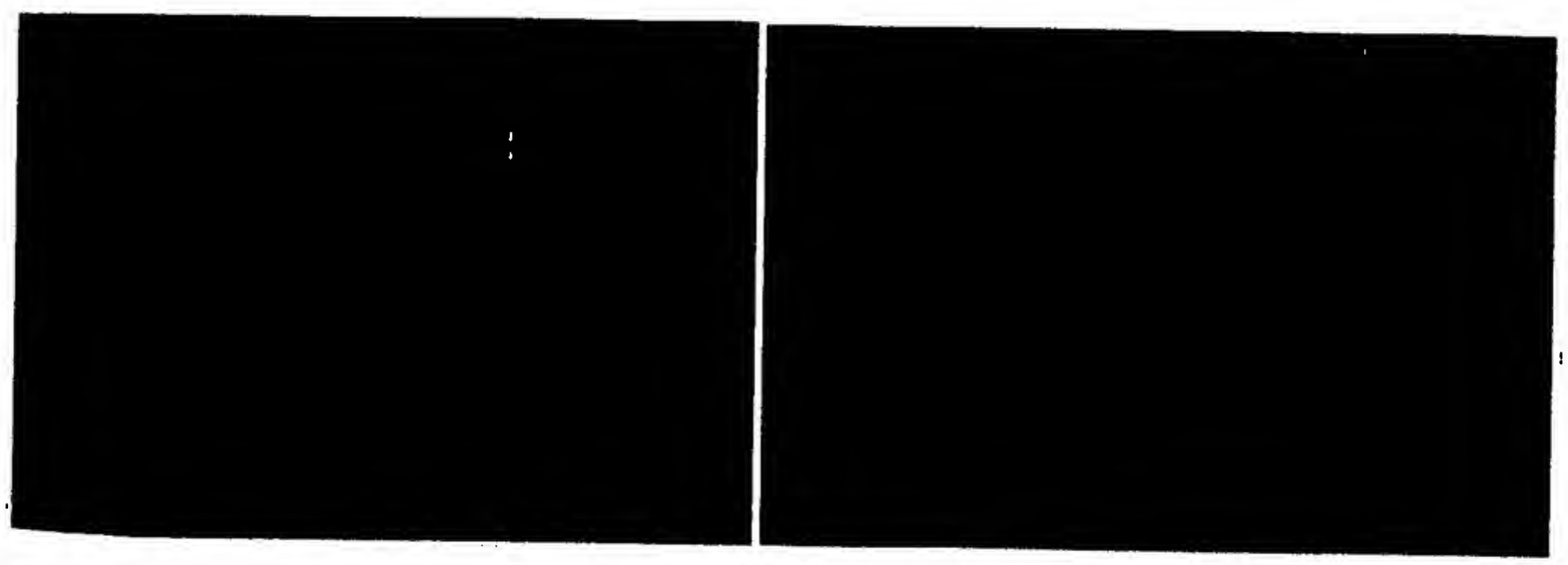

Figure 5A

EGFP-Lgs

Figure 5B

EGFP-Lgs + pcDNA3-Arm-NLS

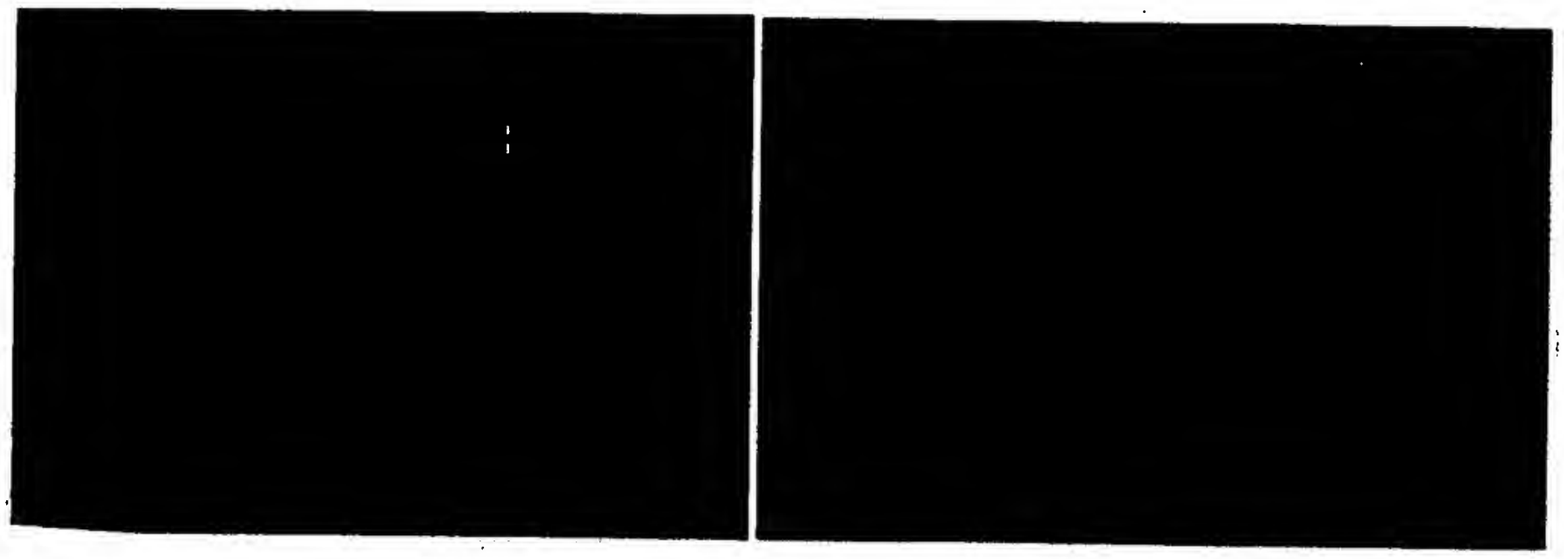

Figure 5C

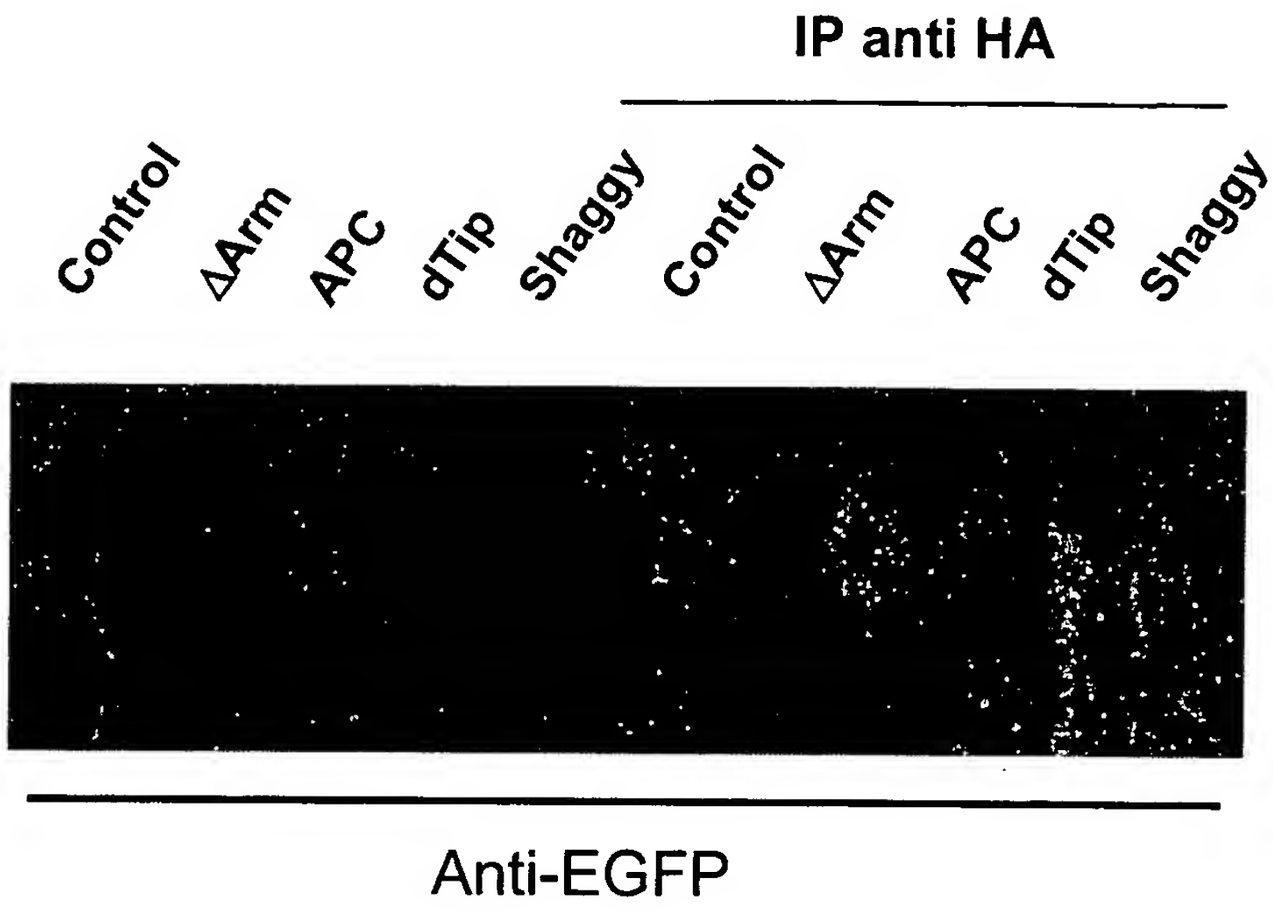
IP anti HA
Control
ΔArm
APC
dTip
Shaggy
Control
ΔArm
APC
dTip
Shaggy
Anti-EGFP

Figure 5D

		BAIT fusions: pLex						
		Lgs 1-1464	BCL9 199-392	BCL9 1-1426	Dco+	ΔArmC	Δß-Cat	Pan
PREY fusions: pJG4-5	lgs364-555					+		
	lgs1-385					-		
	lgs1-732					+		
	lgs364-1090					+		
	lgs726-1464					-		
	lgs1-1464				-	+	n.d.	+
	BCL9 199-392					+	n.d.	
	BCL91-1426					+	+	
	Dco+	-						
	DAxin	(+)			-	+		
	ΔArmC	+	+	+				+
	ß-Cat	+	+	+				
	Pan	+				+		
	pJG4-5	-	-	-		-	-	

+: interaction seen in yeast two-hybrid assay
-: no interaction seen in yeast two-hybrid assay
n.d.: not done
numberings refer to amino acid positions.

Figure 5E

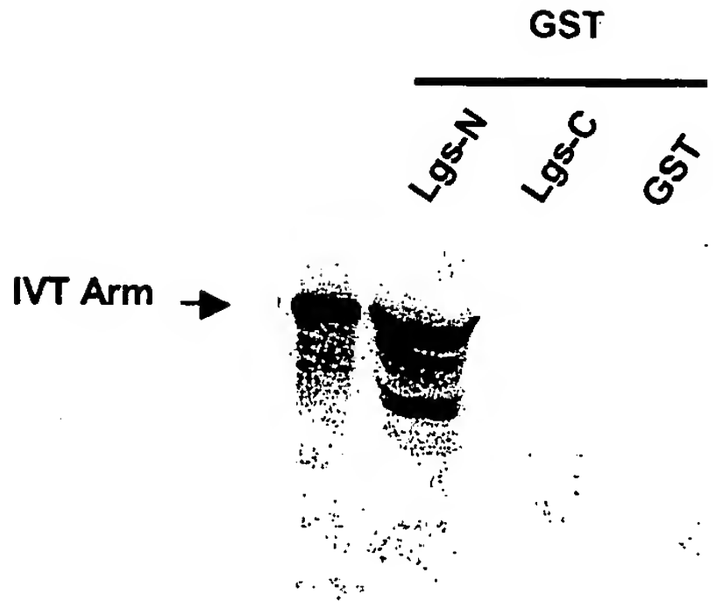

Figure 5F

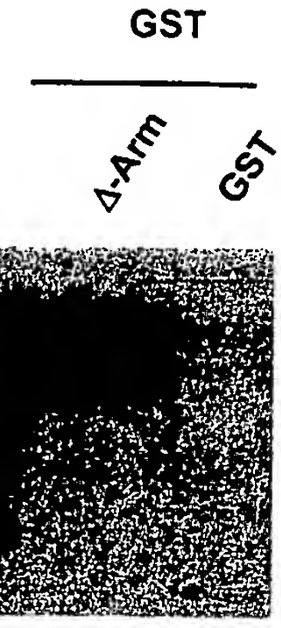

Figure 5G

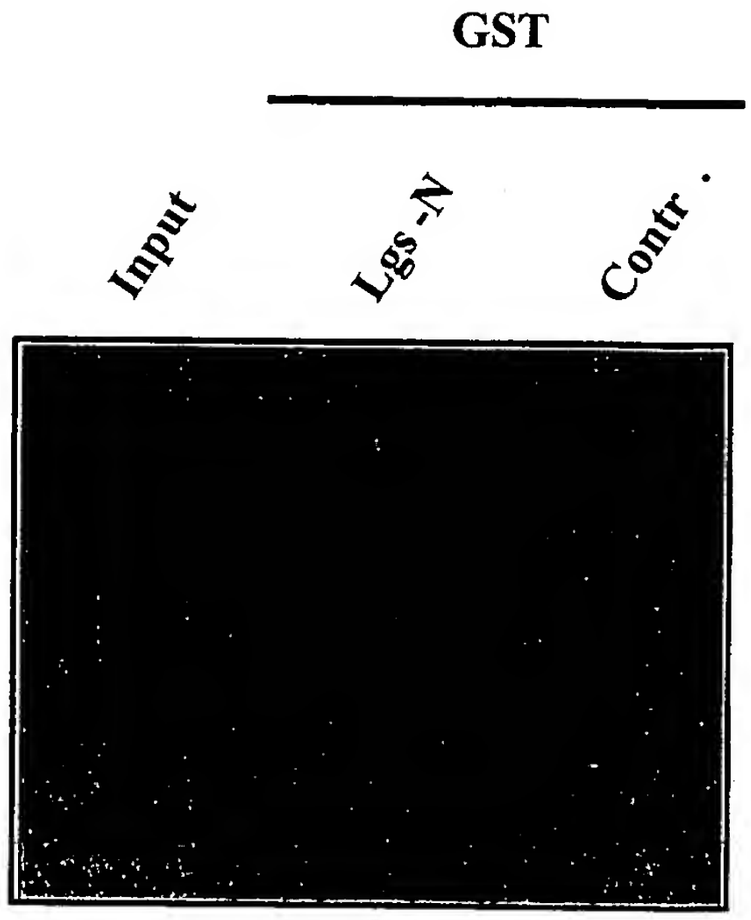

FIG. 6

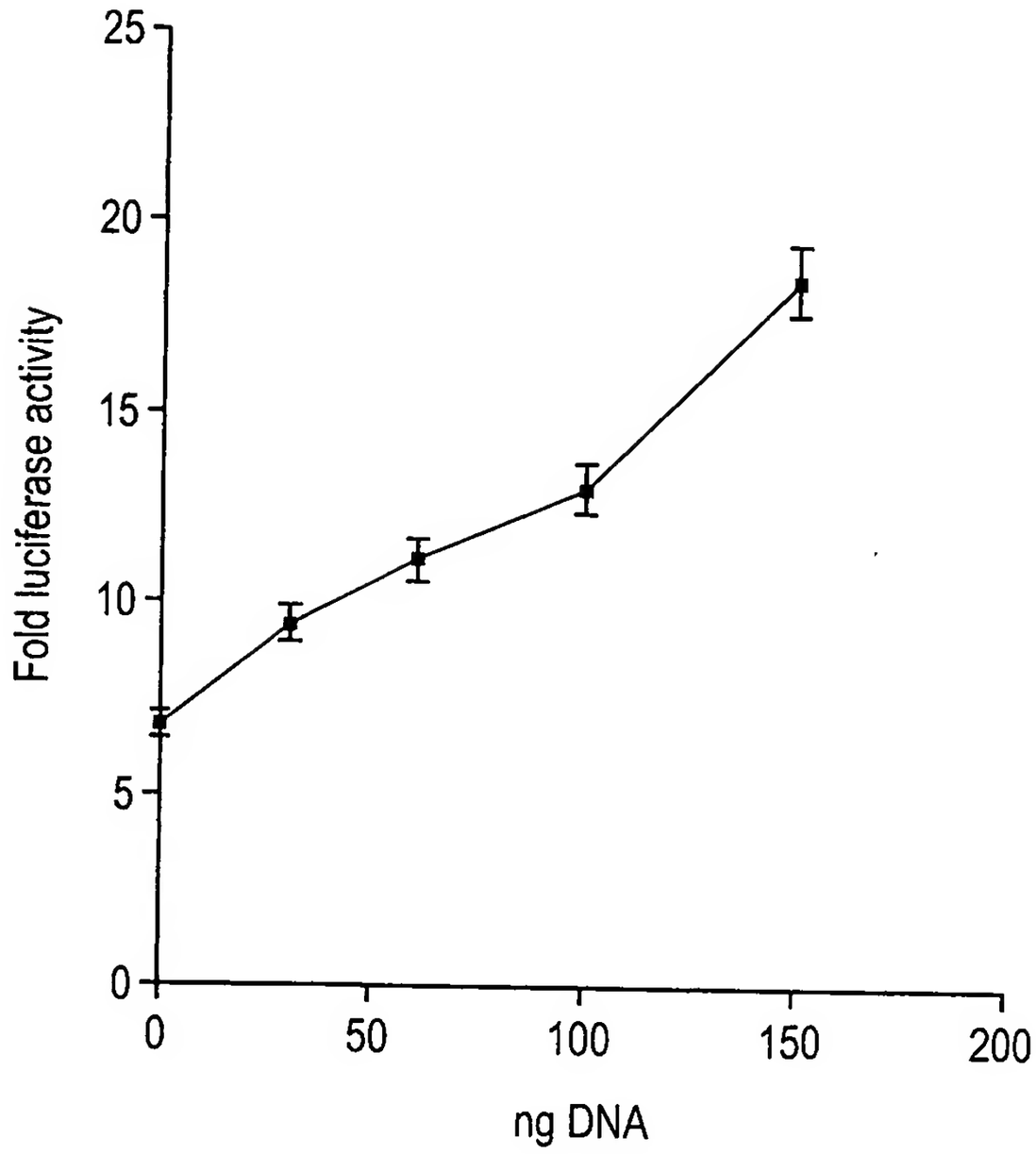

FIG. 7A

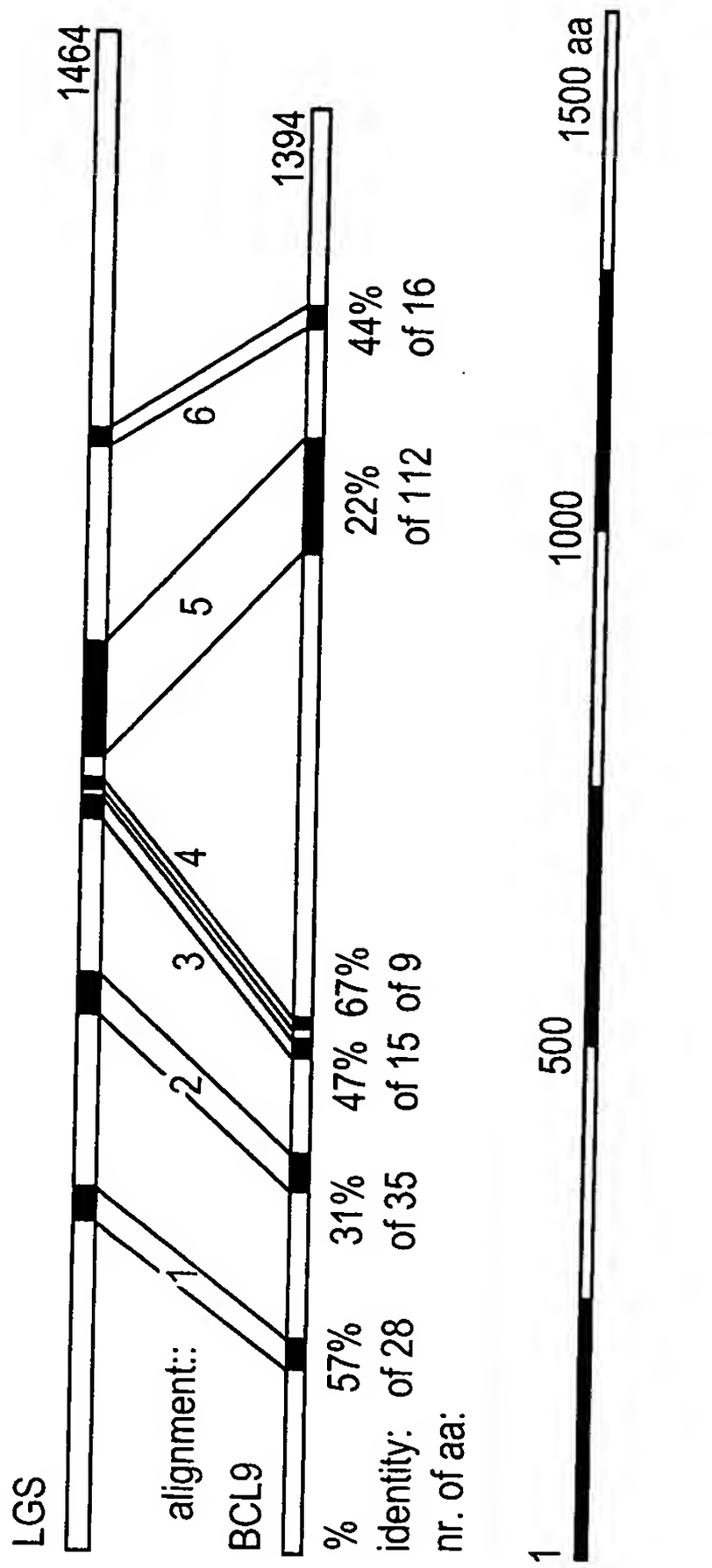
LGS
alignment::
BCL9
% identity:
nr. of aa:
1
500
1000
1500 aa
1464
1394
31% of 35
47% of 15
67% of 9
22% of 112
44% of 16
57% of 28
1
2
3
4
5
6

FIG. 7B

Sequence homology domain 1:57.1% identity in 28 aa

```
        320        330        340
LGS     IFVFSTQLANKGAESVLSGQFQTIIAYH
        ..:::::.:::.::.:: :: .:::...:
BCL9    VYVFSTEMANKAAEAVLKGQVETIVSFH
         180        190        200
```

Sequence homology domain 2:31.4% identity in 35 aa

```
          520        530        540
LGS     ENLTPQQRQHREEQLAKIKKMNQFLFPENENSVGA
        ..:...: .:::  :  .. ... ::::.. . .::
BCL9    DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA
       350        360        370        380
```

Sequence homology domain 3:46.7% identity in 15 aa

```
          710        720
LGS     QMEWSKIQHQFFEER
        :..: :.:..:.::.
BCL9    QIAWLKLQQEFYEEK
       470        480
```

Sequence homology domain 4:66.6% identity in 9 aa

```
           760
LGS     LQGPPPPYH
        ..:::::::.
BCL9    VRGPPPPYQ
               520
```

Sequence homology domain 5:22.3% identity in 112 aa

```
        770        780        790        800        810        820
LGS     SASVPIATQSPNPSSPNNLSLPSPRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQA
        ... :.:.:... . :..:. ..: : ..    :. :. :.   . .:  . ...:.  ..
BCL9    GPPPPTASQPASVNIPGSLPSSTPYTMPPEPTLSQNPLSIM-MSRMSKFAMPSSTPLYHD
       970        980        990       1000       1010       1020

        830        840        850        860        870
LGS     GTTTVLSANKNCFQADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSP
        .. :: :.. .  .: .:. .. :    . : ..   .  ..:: .:.. :::
BCL9    AIKTVASSDDDSPPARSPNLPSMNNMPGMGINTQNPRISGPNPVVPMPTLSP
       1030       1040       1050       1060       1070
```

Sequence homology domain 6:43.8% identity in 16 aa

```
             1080
LGS     NPKMCVAGGPNGPPGF
        .. .: .::::.:: .:

BCL9    DAALCKPGGPGGPDSF
      1190       1200
```

Figure 8A

ATGCATTCCAGTAACCCTAAAGTGAGGAGCTCTCCATCAGGAAACACACA
GAGTAGCCCTAAGTCAAAGCAGGAGGTGATGGTCCGTCCCCCTACAGTGA
TGTCCCCATCTGGAAACCCCCAGCTGGATTCCAAATTCTCCAATCAGGGT
AAACAGGGGGGCTCAGCCAGCCAATCCCAGCCATCCCCCTGTGACTCCAA
GAGTGGGGGCCATACCCCTAAAGCACTCCCTGGCCCAGGTGGGAGCATGG
GGCTGAAGAATGGGGCTGGAAATGGTGCCAAGGGCAAGGGGAAAAGGGAG
CGAAGTATTTCCGCCGACTCCTTTGATCAGAGAGATCCTGGGACTCCAAA
CGATGACTCTGACATTAAAGAATGTAATTCTGCTGACCACATAAAGTCCC
AGGATTCCCAGCACACACCACACTCGATGACCCCATCAAATGCTACAGCC
CCCAGGTCTTCTACCCCCTCCCATGGCCAAACTACTGCCACAGAGCCCAC
ACCTGCTCAGAAGACTCCAGCCAAAGTGGTGTACGTGTTTTCTACTGAGA
TGGCCAATAAAGCTGCAGAAGCTGTTTTGAAGGGCCAGGTTGAAACTATC
GTCTCTTTCCACATCCAGAACATTTCTAACAACAAGACAGAGAGAAGCAC
AGCGCCTCTGAACACACAGATATCTGCCCTTCGGAATGATCCGAAACCTC
TCCCACAACAGCCCCCAGCTCCGGCCAACCAGGACCAGAATTCTTCCCAG
AATACCAGACTGCAGCCAACTCCACCCATTCCGGCACCAGCACCCAAGCC
TGCCGCACCCCCACGTCCCCTGGACCGGGAGAGTCCTGGGGTAGAAAACA
AACTGATTCCTTCTGTAGGAAGTCCTGCCAGCTCCACTCCACTGCCCCCA
GATGGTACTGGGCCCAACTCAACTCCCAACAATAGGGCAGTGACCCCTGT
CTCCCAGGGGAGCAATAGCTCTTCAGCAGATCCCAAAGCCCCTCCGCCTC
CACCAGTGTCCAGTGGCGAGCCCCCCACACTGGGAGAGAATCCCGATGGC
CTATCTCAGGAGCAGCTGGAGCACCGGGAGCGCTCCTTACAAACTCTCAG
AGATATCCAGCGCATGCTTTTTCCTGATGAGAAAGAATTCACAGGAGCAC
AAAGTGGGGGACCGCAGCAGAATCCTGGGGTATTAGATGGGCCTCAGAAA
AAACCAGAAGGGCCAATACAGGCCATGATGGCCCAATCCCAAAGCCTAGG
TAAGGGACCTGGGCCCCGGACAGACGTGGGAGCTCCATTTGGCCCTCAAG
GACATAGAGATGTACCCTTTTCTCCAGATGAAATGGTTCCACCTTCTATG
AACTCCCAGTCTGGGACCATAGGACCCGACCACCTTGACCATATGACTCC
CGAGCAGATAGCGTGGCTGAAACTGCAGCAGGAGTTTTATGAAGAGAAGA
GGAGGAAGCAGGAACAAGTGGTTGTCCAGCAGTGTTCCCTCCAGGACATG
ATGGTCCATCAGCACGGGCCTCGGGGAGTGGTCCGAGGACCCCCCCCTCC
ATACCAGATGACCCCTAGTGAAGGCTGGGCACCTGGGGGTACAGAGCCAT
TTTCTGATGGTATCAACATGCCACATTCTCTGCCCCCGAGGGGCATGGCT
CCCCACCCCAACATGCCAGGGAGCCAGATGCGCCTCCCTGGATTTGCAGG
CATGATAAACTCTGAAATGGAAGGGCCGAATGTCCCCAACCCTGCATCTA
GACCAGGTCTTTCTGGAGTCAGTTGGCCAGATGATGTGCCAAAAATCCCA
GATGGTCGAAATTTTCCTCCTGGCCAGGGCATTTTCAGCGGTCCTGGCCG
AGGGGAACGCTTCCCAAACCCCCAAGGATTGTCTGAAGAGATGTTTCAGC
AGCAGCTGGCAGAGAAACAGCTGGGTCTCCCCCCAGGGATGGCCATGGAA
GGCATCAGGCCCAGCATGGAGATGAACAGGATGATTCCAGGCTCCCAGCG
CCACATGGAGCCTGGGAATAACCCCATTTTCCCTCGAATACCAGTTGAGG
GCCCTCTGAGTCCTTCTAGGGGTGACTTTCCAAAAGGAATTCCCCCACAG

Figure 8A (Cont.)

ATGGGCCCTGGTCGGGAACTTGAGTTTGGGATGGTTCCTAGTGGGATGAA
GGGAGATGTCAATCTAAATGTCAACATGGGATCCAACTCTCAGATGATAC
CTCAGAAGATGAGAGAGGCTGGGGCGGGCCCTGAGGAGATGCTGAAATTA
CGCCCAGGTGGCTCAGACATGCTGCCTGCTCAGCAGAAGATGGTGCCACT
GCCATTTGGTGAGCACCCCCAGCAGGAGTATGGCATGGGCCCCAGACCAT
TCCTTCCCATGTCTCAGGGTCCAGGCAGCAACAGTGGCTTGCGGAATCTC
AGAGAACCAATTGGGCCCGACCAGAGGACTAACAGCCGGCTCAGTCATAT
GCCACCACTACCTCTCAACCCTTCCAGTAACCCCACCAGCCTCAACACAG
CTCCTCCAGTTCAGCGCGGCCTGGGGCGGAAGCCCTTGGATATATCTGTG
GCAGGCAGCCAGGTGCATTCCCCAGGCATTAACCCTCTGAAGTCTCCCAC
GATGCACCAAGTCCAGTCACCAATGCTGGGCTCGCCCTCGGGGAACCTCA
AGTCCCCCCAGACTCCATCGCAGCTGGCAGGCATGCTGGCGGGCCCAGCT
GCTGCTGCTTCCATTAAGTCCCCCCCTGTTTTGGGGTCTGCTGCTGCTTC
ACCTGTCCACCTCAAGTCTCCATCACTTCCTGCCCCGTCACCTGGATGGA
CCTCTTCTCCAAAACCTCCCCTTCAGAGTCCTGGGATCCCTCCAAACCAT
AAAGCACCCCTCACCATGGCCTCCCCAGCCATGCTGGGAAATGTAGAGTC
AGGTGGCCCCCCACCTCCTACAGCCAGCCAGCCTGCCTCTGTGAATATCC
CTGGAAGTCTTCCCTCTAGTACACCTTATACCATGCCTCCAGAGCCAACC
CTTTCCCAGAACCCACTCTCTATTATGATGTCTCGAATGTCCAAGTTTGC
AATGCCCAGTTCCACCCCGTTATACCATGATGCTATCAAGACTGTGGCCA
GCTCAGATGACGACTCCCCTCCAGCTCGTTCTCCCAACTTGCCATCAATG
AATAATATGCCAGGAATGGGCATTAATACACAGAATCCTCGAATTTCAGG
TCCAAACCCCGTGGTTCCGATGCCAACCCTCAGCCCAATGGGAATGACCC
AGCCACTTTCTCACTCCAATCAGATGCCCTCTCCAAATGCCGTGGGACCC
AACATACCTCCTCATGGGGTCCCAATGGGGCCTGGCTTGATGTCACACAA
TCCTATCATGGGGCATGGGTCCCAGGAGCCACCGATGGTACCTCAAGGAC
GGATGGGCTTCCCCCAGGGCTTCCCTCCAGTACAGTCTCCCCCACAGCAG
GTTCCATTCCCTCACAATGGCCCCAGTGGGGGGCAGGGCAGCTTCCCAGG
AGGGATGGGTTTCCCAGGAGAAGGCCCCCTTGGCCGCCCCAGCAACCTGC
CCCAAAGTTCAGCAGATGCAGCACTTTGCAAGCCTGGAGGCCCCGGGGGT
CCTGACTCCTTCACTGTCCTGGGGAACAGCATGCCTTCGGTGTTTACAGA
CCCAGATCTGCAGGAGGTCATCCGACCTGGAGCCACCGGAATACCTGAGT
TTGATCTATCCCGCATTATTCCATCTGAGAAGCCCAGCCAGACGCTGCAA
TATTTCCCTCGAGGGGAAGTTCCAGGCCGTAAACAGCCCCAGGGTCCTGG
ACCTGGGTTTTCACACATGCAGGGGATGATGGGCGAACAAGCCCCCAGAA
TGGGACTAGCATTACCTGGCATGGGAGGTCCAGGGCCAGTGGGAACTCCG
GACATCCCTCTTGGTACAGCTCCATCCATGCCAGGCCACAACCCCATGAG
ACCACCAGCCTTTCTCCAACAAGGCATGATGGGACCTCACCATCGGATGA
TGTCACCAGCACAATCTACAATGCCCGGCCAGCCCACCCTGATGAGCAAT
CCAGCTGCTGCCGTGGGCATGATTCCTGGCAAGGATCGGGGGCCTGCCGG
GCTCTACACCCACCCTGGGCCTGTGGGCTCTCCAGGCATGATGATGTCCA
TGCAGGGCATGATGGGACCCCAACAGAACATCATGATCCCCCCACAGATG
AGGCCCCGGGGCATGGCTGCTGACGTGGGCATGGGTGGATTTAGCCAAGG
ACCTGGCAACCCAGGAAACATGATGTTTTAA

Figure 8B

MHSSNPKVRSSPSGNTQSSPKSKQEVMVRPPTVMSPSGNPQLDSKFSNQG
KQGGSASQSQPSPCDSKSGGHTPKALPGPGGSMGLKNGAGNGAKGKGKRE
RSISADSFDQRDPGTPNDDSDIKECNSADHIKSQDSQHTPHSMTPSNATA
PRSSTPSHGQTTATEPTPAQKTPAKVVYVFSTEMANKAAEAVLKGQVETI
VSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQ
NTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPP
DGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTLGENPDG
LSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQSGGPQQNPGVLDGPQK
KPEGPIQAMMAQSQSLGKGPGPRTDVGAPFGPQGHRDVPFSPDEMVPPSM
NSQSGTIGPDHLDHMTPEQIAWLKLQQEFYEEKRRKQEQVVVQQCSLQDM
MVHQHGPRGVVRGPPPPYQMTPSEGWAPGGTEPFSDGINMPHSLPPRGMA
PHPNMPGSQMRLPGFAGMINSEMEGPNVPNPASRPGLSGVSWPDDVPKIP
DGRNFPPGQGIFSGPGRGERFPNPQGLSEEMFQQQLAEKQLGLPPGMAME
GIRPSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGPLSPSRGDFPKGIPPQ
MGPGRELEFGMVPSGMKGDVNLNVNMGSNSQMIPQKMREAGAGPEEMLKL
RPGGSDMLPAQQKMVPLPFGEHPQQEYGMGPRPFLPMSQGPGSNSGLRNL
REPIGPDQRTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRGLGRKPLDISV
AGSQVHSPGINPLKSPTMHQVQSPMLGSPSGNLKSPQTPSQLAGMLAGPA
AAASIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSSPKPPLQSPGIPPNH
KAPLTMASPAMLGNVESGGPPPPTASQPASVNIPGSLPSSTPYTMPPEPT
LSQNPLSIMMSRMSKFAMPSSTPLYHDAIKTVASSDDDSPPARSPNLPSM
NNMPGMGINTQNPRISGPNPVVPMPTLSPMGMTQPLSHSNQMPSPNAVGP
NIPPHGVPMGPGLMSHNPIMGHGSQEPPMVPQGRMGFPQGFPPVQSPPQQ
VPFPHNGPSGGQGSFPGGMGFPGEGPLGRPSNLPQSSADAALCKPGGPGG
PDSFTVLGNSMPSVFTDPDLQEVIRPGATGIPEFDLSRIIPSEKPSQTLQ
YFPRGEVPGRKQPQGPGPGFSHMQGMMGEQAPRMGLALPGMGGPGPVGTP
DIPLGTAPSMPGHNPMRPPAFLQQGMMGPHHRMMSPAQSTMPGQPTLMSN
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RPRGMAADVGMGGFSQGPGNPGNMMF*

FIG. 9

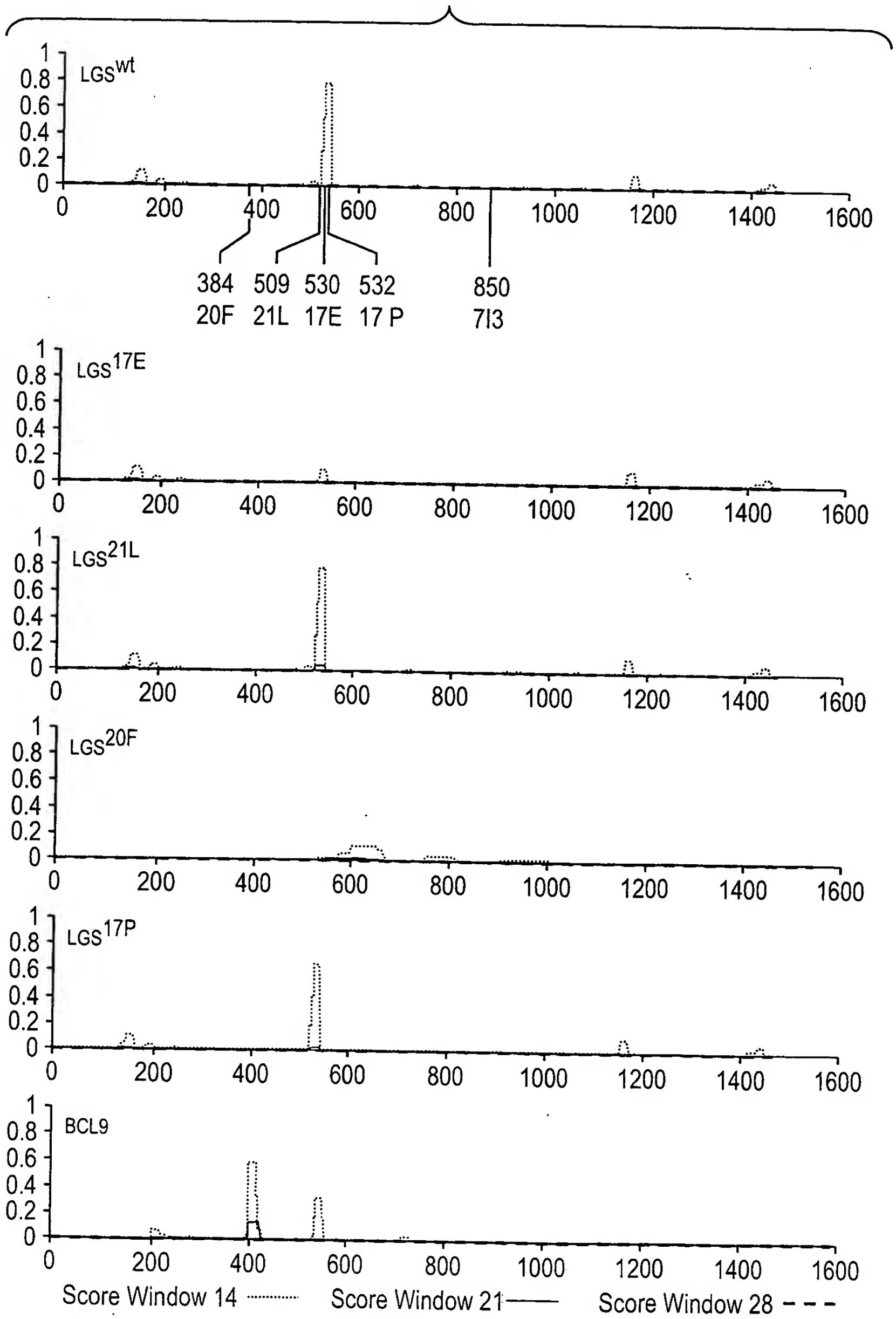
384 509 530 532 850
20F 21L 17E 17 P 7I3
LGS^wt
LGS^17E
LGS^21L
LGS^20F
LGS^17P
BCL9
0 0.2 0.4 0.6 0.8 1
0 200 400 600 800 1000 1200 1400 1600
Score Window 14
Score Window 21
Score Window 28

Figure 10A

ATGGCCTGCTTCCCATCCCCTGCTGCCATCTCCTGCACCCTTAGGGCACAGTGGGCATCT
CGGGAGCTGCTCAGCGGACAGACTAGGGTTACCCCCACCCCAGGAGGAGAGAAGCTCCAG
GGAGCCCGCCGCTGTCCCCCGCGGTCATTGCCCCCTGCCCCAGCCAAGCCAATGCACCCA
GAAAATAAATTGACCAATCATGGCAAGACAGGGAATGGCGGGGCCCAATCTCAGCACCAG
AATGTGAACCAAGGACCCACCTGCAACGTGGGCTCGAAGGGCGTGGGGGCGGGGAACCAT
GGGGCCAAGGCCAACCAGATCTCGCCTAGCAACTCAAGTCTGAAGAACCCCCAGGCAGGG
GTGCCCCCTTTCAGCTCGCTCAAGGGCAAGGTGAAGAGGGACCGGAGTGTGTCTGTGGAC
TCTGGAGAGCAGCGAGAGGCTGGGACCCCATCCCTGGATTCAGAGGCCAAAGAGGTGGCG
CCGCGGAGTAAGCGGCGCTGTGTGCTGGAGCGGAAGCAGCCGTACAGTGGGGACGAATGG
TGCTCTGGACCGGACAGTGAGGAGGACGACAAGCCCATTGGGGCCACCCACAAAGCTGCT
TTCAAAGAAGACGGCTTTCAGGACAAGGCATCACACTTCTTCTCCAGCACGTACAGTCCT
GAAACCTCCAGGAGGAAGCTGCCCCAAGCCCCGAAGGCTTCCTTCCTGGGGCAGCAGGGC
CGAGTCATTTGGAAACCTCTCTCGGAGGAGCTCCGTGATCAAGGTGCAGATGCGGCAGGT
GGGCCGGCCTCAATCATGTCTCCAATCGCGACGGTGAATGCGAGTGGCTTGTCCAAAGAG
CAGCTGGAGCATCGGGAACGGTCCCTCCAGACGCTGCGAGACATTGAGCGACTGCTGCTC
CGCAGCGGAGAGACTGAGCCCTTCCTCAAGGGGGCCCCCAGGAGGAGCGGCGGGCTGAAG
AAATATGAGGAACCCTTGCAGTCCATGATTTCACAGACACAGAGCCTAGGGGGCCCCCCG
CTGGAGCATGAAGTGCCTGGGCACCCCCCGGGTGGGGACATGGGGCAGCAGATGAACATG
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CAGGAGGAGTACTACGAAGAGAAACGGCGGAAAGAGGAACAGATTGGGCTGCATGGGAGC
CGTCCTCTGCAGGACATGATGGGCATGGGGGGCATGATGGTGAGGGGGCCCCCGCCTCCT
TACCACAGCAAGCCTGGGGATCAGTGGCCACCTGGAATGGGTGCGCAGCTGCGGGGGCCC
ATGGATGTTCAAGATCCCATGCAGCTCCGGGGCGGACCTCCCTTTCCTGGGCCCCGTTTC
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CCCCCTATGGGGGGACCCAGCAATTTTGCCCAGAACACCATGCCCTACCCAGGTGGGCAG
GGTGAGGCGGAGCGATTCATGACTCCCCGGGTCCGTGAGGAGCTGCTGCGGCACCAGCTG
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CAGAGCATGGAGATGGAGCGGATGATGCAGGCGCACCGACAGATGGATCCTGCCATGTTT
CCCGGGCAGATGGCTGGTGGTGAGGGCCTGGCGGGCACTCCCATGGGCATGGAGTTTGGT
GGAGGCCGGGGCCTCCTGAGCCCTCCCATGGGGCAGTCTGGGCTGAGGGAGGTGGACCCA
CCCATGGGGCCAGGCAACCTCAACATGAACATGAATGTCAACATGAACATGAACATGAAC
CTGAACGTGCAGATGACCCCGCAGCAGCAGATGCTGATGTCGCAGAAGATGCGGGGCCCT
GGGGACTTGATGGGGCCCCAGGGCCTCAGTCCTGAGGAGATGGCCCGGGTTCGGGCCCAG
AACAGCAGTGGCATGGTGCCCTTGCCTTCTGCCAACCCGCCAGGACCTCTCAAGTCGCCC
CAGGTCCTCGGCTCCTCCCTCAGTGTCCGTTCACCCACTGGCTCGCCCAGCAGGCTCAAG
TCTCCTTCCATGGCGGTGCCTTCTCCAGGCTGGGTTGCCTCACCCAAGACGGCCATGCCC
AGCCCGGGGGTCTCCCAGAACAAGCAGCCGCCTCTCAACATGAACTCTTCCACCACCCTG
AGCAACATGGAACAGGACCCCACACCTTCCCAGAACCCCCTGTCACTGATGATGACCCAG
ATGTCCAAGTACGCCATGCCCAGCTCCACCCCGCTCTACCACAATGCCATCAAGACCATC
GCCACCTCAGACGACGAGCTGCTGCCCGACCGGCCCCTGCTGCCCCCCCCACCACCACCG
CAGGGCTCCGGGCCAGGTGGCCCCGACTCCCTGAATGCCCCCTGTGGCCCAGTGCCCAGC
TCCTCCCAGATGATGCCCTTCCCCCCTCGGCTGCAGCAGCCCCATGGTGCCATGGCCCCC
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CCTCCCGAGGACCTGCCCAACCAGCCGCCAGGCCCCATGCCTCCCCAGCAGCACCTGATG
GGCAAAGCCATGGCTGGGCGCATGGGCGACGCATACCCACCGGGTGTGCTCCCTGGGGTG
GCATCAGTGCTGAACGACCCCGAGCTGAGCGAGGTGATCCGGCCCACCCCAACGGGGATC
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CTGCAGAACATGATGGCGGAGCAGACTCCCTCTCGGCCTCCCAACCTCCCAGGCCAGCAG
GGCGATCGGCCGCTGGTGGTGGTGATACCGGGTACCCGGGCTATGGCGCCGGCGCAGCGC
TGCCCTCTGTGCCGCCAGACCTTCTTCTGTGGTCGCGGGCACGTTTACAGCCGCAAGCAC
CAGCGGCAGCTGAAGGAGGCTTTGGAGAGGCTCCTGCCCCAGGTGGAGGCGGCCCGCAAG
GCCATCCGCGCCGCTCAGGTGGAGCGCTATGTGCCCGAACACGAGCGATGCTGCTGGTGC
CTGTGCTGCGGCTGTGAGGTGCGGGAACACCTGAGCCATGGAAACCTGACGGTGCTGTAC

Figure 10A (Cont.)

GGGGGGCTGCTGGAGCATCTGGCCAGCCCAGAGCACAAGAAAGCAACCAACAAATTCTGG
TGGGAGAACAAAGCTGAGGTCCAGATGAAAGAGAAGTTTCTGGTCACTCCCCAGGATTAT
GCGCGATTCAAGAAATCCATGGTGAAAGGTTTGGATTCCTATGAAGAAAAGGAGGATAAA
GTGATCAAGGAGATGGCAGCTCAGATCCGTGAGGTGGAGCAGAGCCGACAGGAGGTGGTT
CGGTCTGTCTTAGAGACAGGTCCCCCAAGATACGCCCTCACAGTCCGGTCCCCCGCCGTC
CTCTCCCGGCGCACGCTCAAGTCCGGTGCCTTCCCCCCGCAGACCCCCGAGGCGCACCCT
CAAGCTCGGTGCCTCTGCGCCCCCCGCAGGGGCGCCCTCAAGCCTGAGCCCCCCGGGCGC
ACCCTCAAGCTCGGTGTACCCCCCCATACCACCCGCAAGGCGCGCCCTCATGCCGCGAAG
ACTTCGCCCCGCCCAAGGTGCACCCGTCAAGCCCCGAATAAAACCCAGTCACTCCAACTT
GCAGGCAAAGCTAGAAAAACTGCGCTGCATTTGCAAACAAAAGCTCTTGTTGGCGATGAC
GATACTGTTTTGGGTGTGAAACTGTCAATTGCTAACTACGATCTGTGA

Figure 10B

FKEDGFQDKASHFFSSTYSPETSRRKLPQAPKASFLGQQGRVIWKPLSEE
LRDQGADAAGGPASIMSPIATVNASGLSKEQLEHRERSLQTLRDIERLLL
RSGETEPFLKGAPRRSGGLKKYEEPLQSMISQTQSLGGPPLEHEVPGHPP
GGDMGQQMNMMIQRLGQDSLTPEQVAWRKLQEEYYEEKRRKEEQIGLHGS
RPLQDMMGMGGMMVRGPPPPYHSKPGDQWPPGMGAQLRGPMDVQDPMQLR
GGPPFPGPRFPGNQIQRVPGFGGMQSMPMEVPMNAMQRPVRPGMGWTEDL
PPMGGPSNFAQNTMPYPGGQGEAERFMTPRVREELLRHQLLEKRSMGMQR
PLGMAGSGMGQSMEMERMMQAHRQMDPAMFPGQMAGGEGLAGTPMGMEFG
GGRGLLSPPMGQSGLREVDPPMGPGNLNMNMNVNMNMNMNLNVQMTPQQQ
MLMSQKMRGPGDLMGPQGLSPEEMARVRAQNSSGMVPLPSANPPGPLKSP
QVLGSSLSVRSPTGSPSRLKSPSMAVPSPGWVASPKTAMPSPGVSQNKQP
PLNMNSSTTLSNMEQDPTPSQNPLSLMMTQMSKYAMPSSTPLYHNAIKTI
ATSDDELLPDRPLLPPPPPPQGSGPGGPDSLNAPCGPVPSSSQMMPFPPR
LQQPHGAMAPTGGGGGGPGLQQHYPSGMALPPEDLPNQPPGPMPPQQHLM
GKAMAGRMGDAYPPGVLPGVASVLNDPELSEVIRPTPTGIPEFDLSRIIP
SEKPSSTLQYFPKSENQPPKAQPPNLHLMNLQNMMAEQTPSRPPNLPGQQ
GDRPLVVVIPGTRAMAPAQRCPLCRQTFFCGRGHVYSRKHQRQLKEALER
LLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLY
GGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKG
LDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLETGPPRYALTVRSPAV
LSRRTLKSGAFPPQTPEAHPQARCLCAPRRGALKPEPPGRTLKLGVPPHT
TRKARPHAAKTSPRPRCTRQAPNKTQSLQLAGKARKTALHLQTKALVGDD
DTVLGVKLSIANYDL

FIG. 11A

FIG. 11B

FIG. 12A

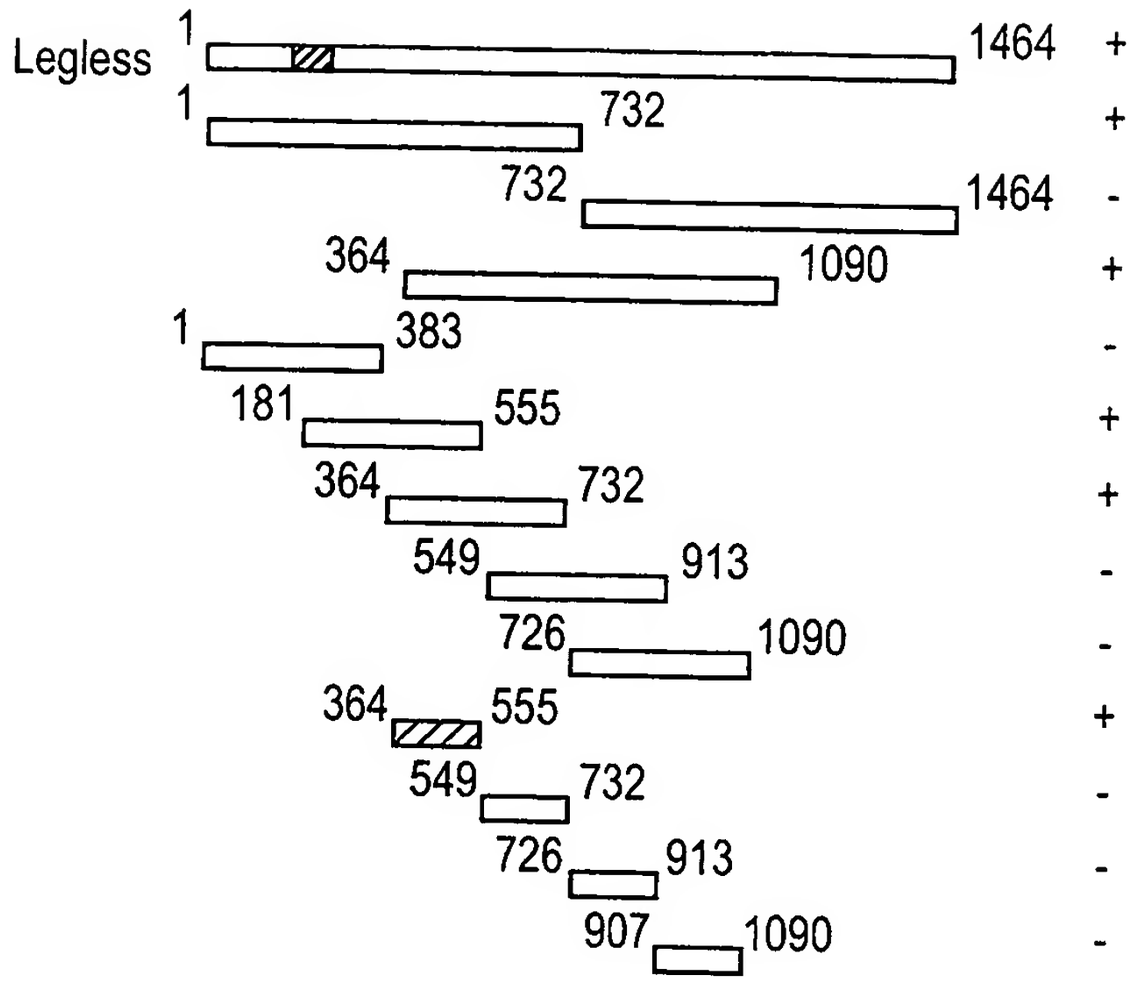

FIG. 12B

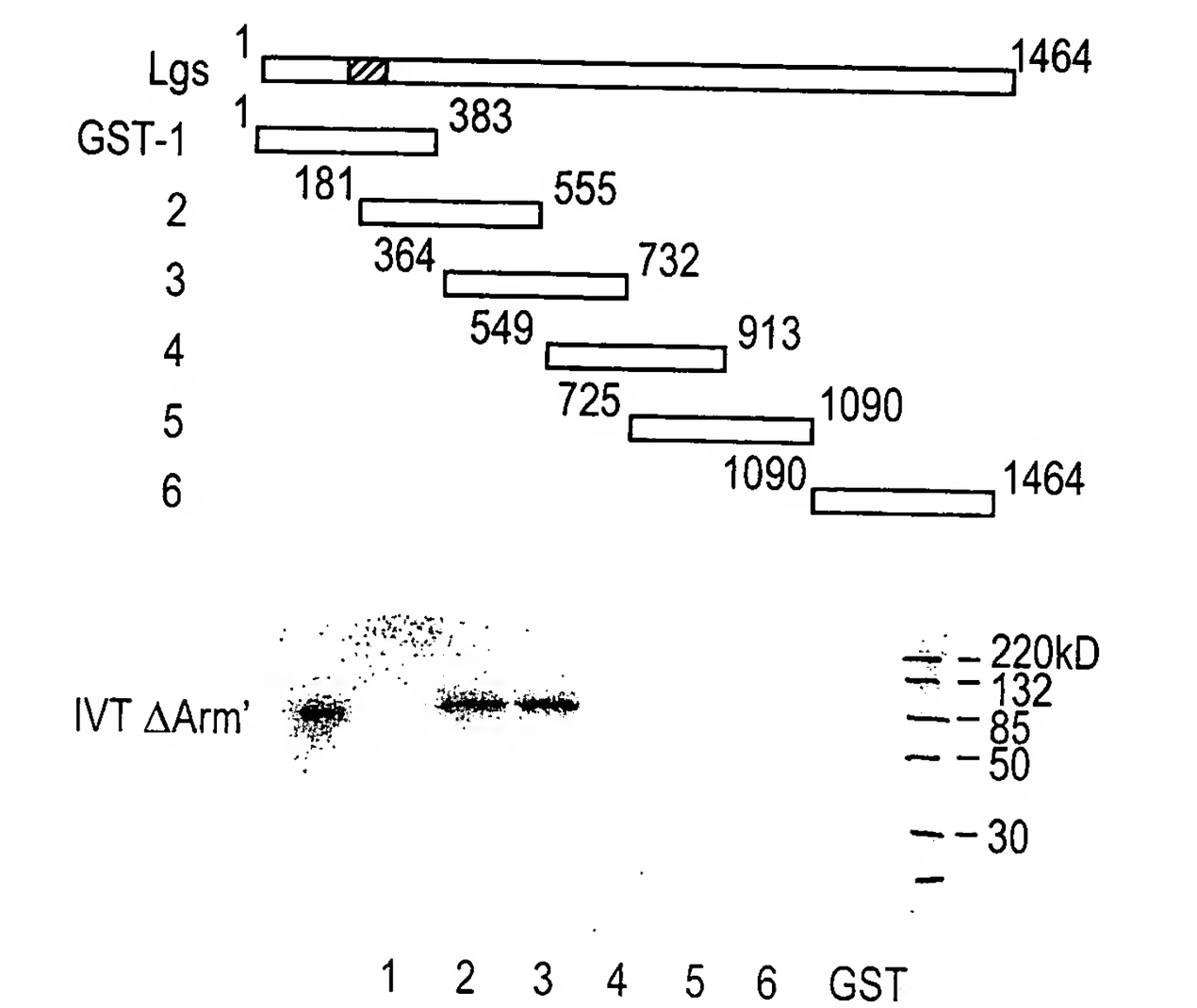

FIG. 12C

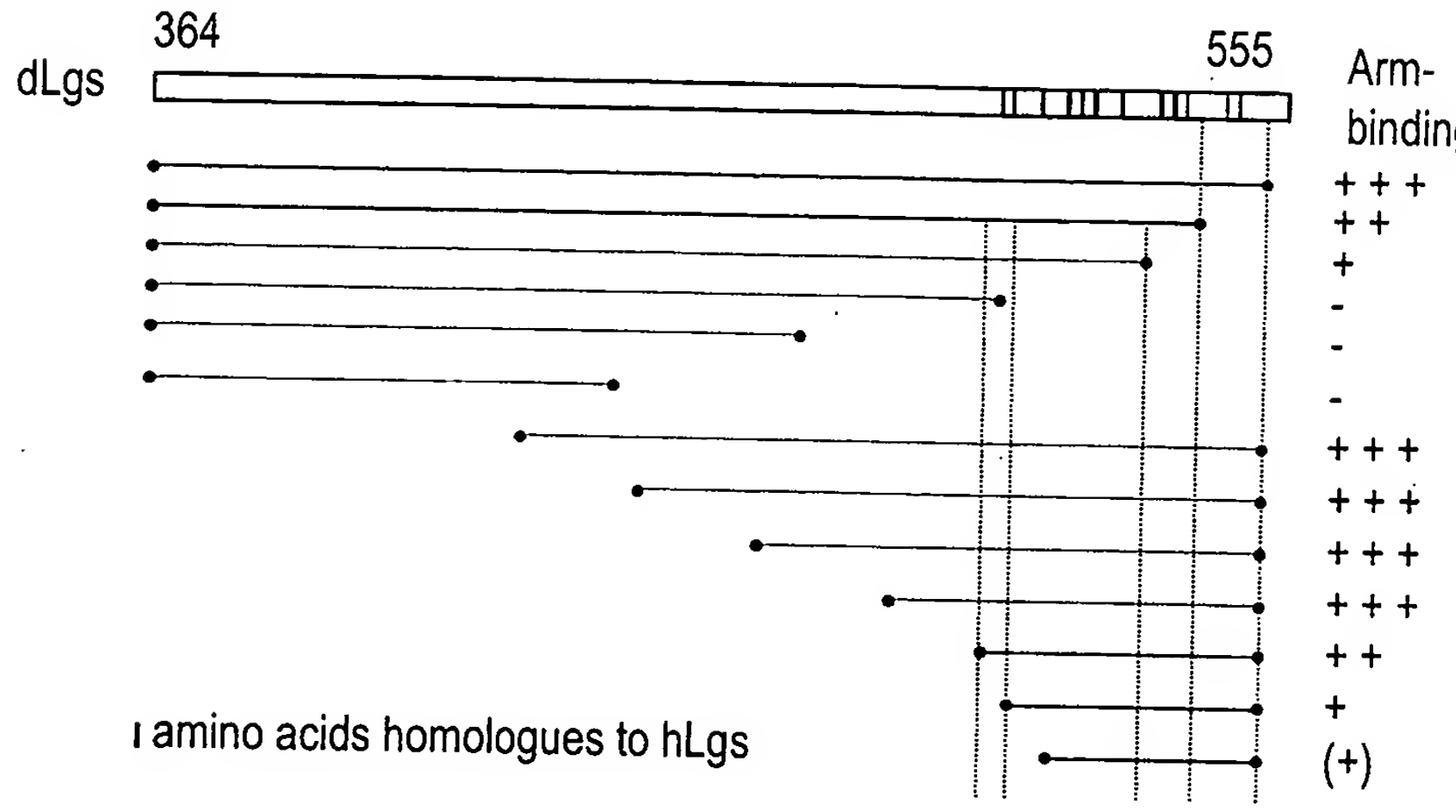

FIG. 12D

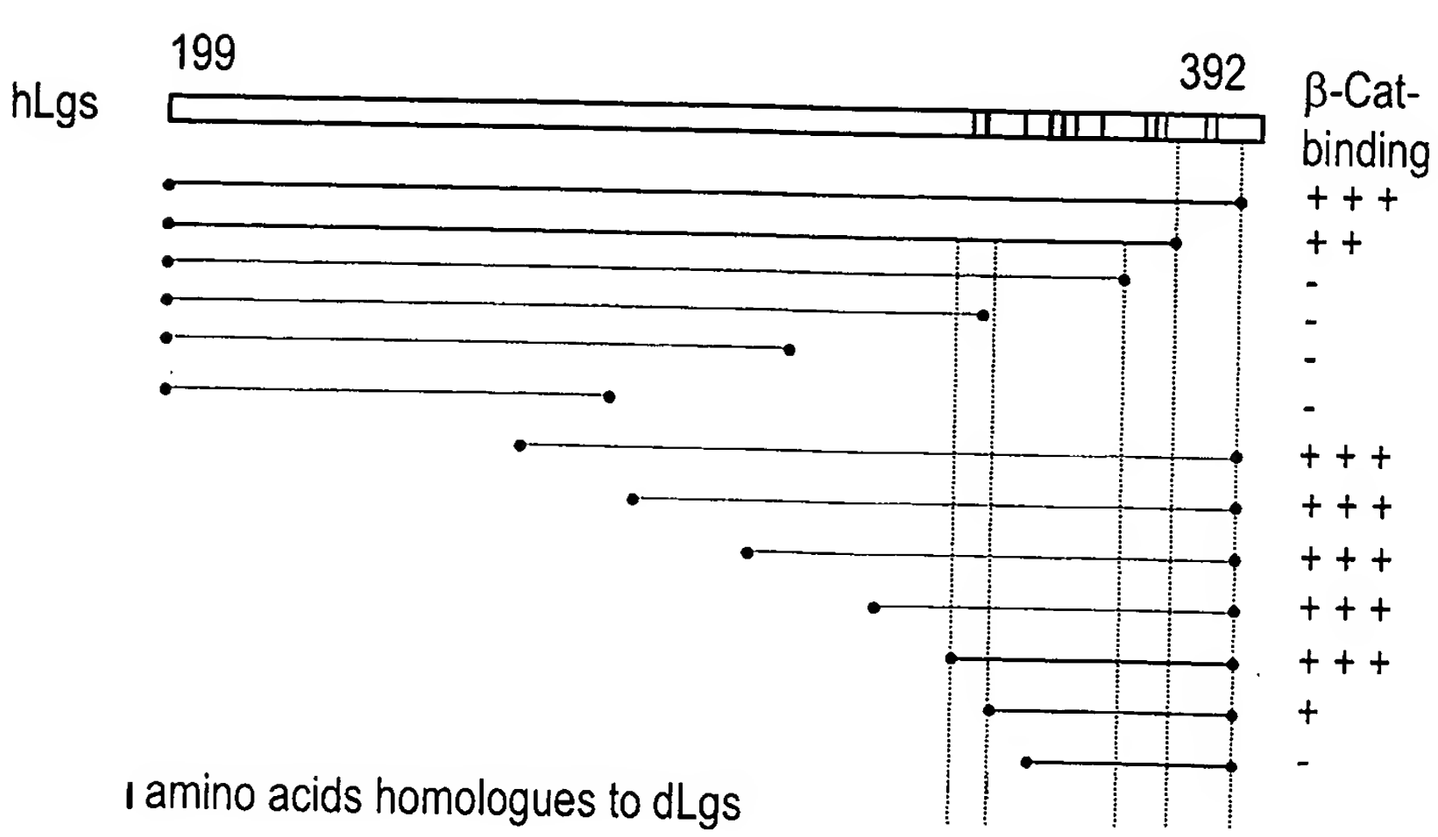

FIG. 12E

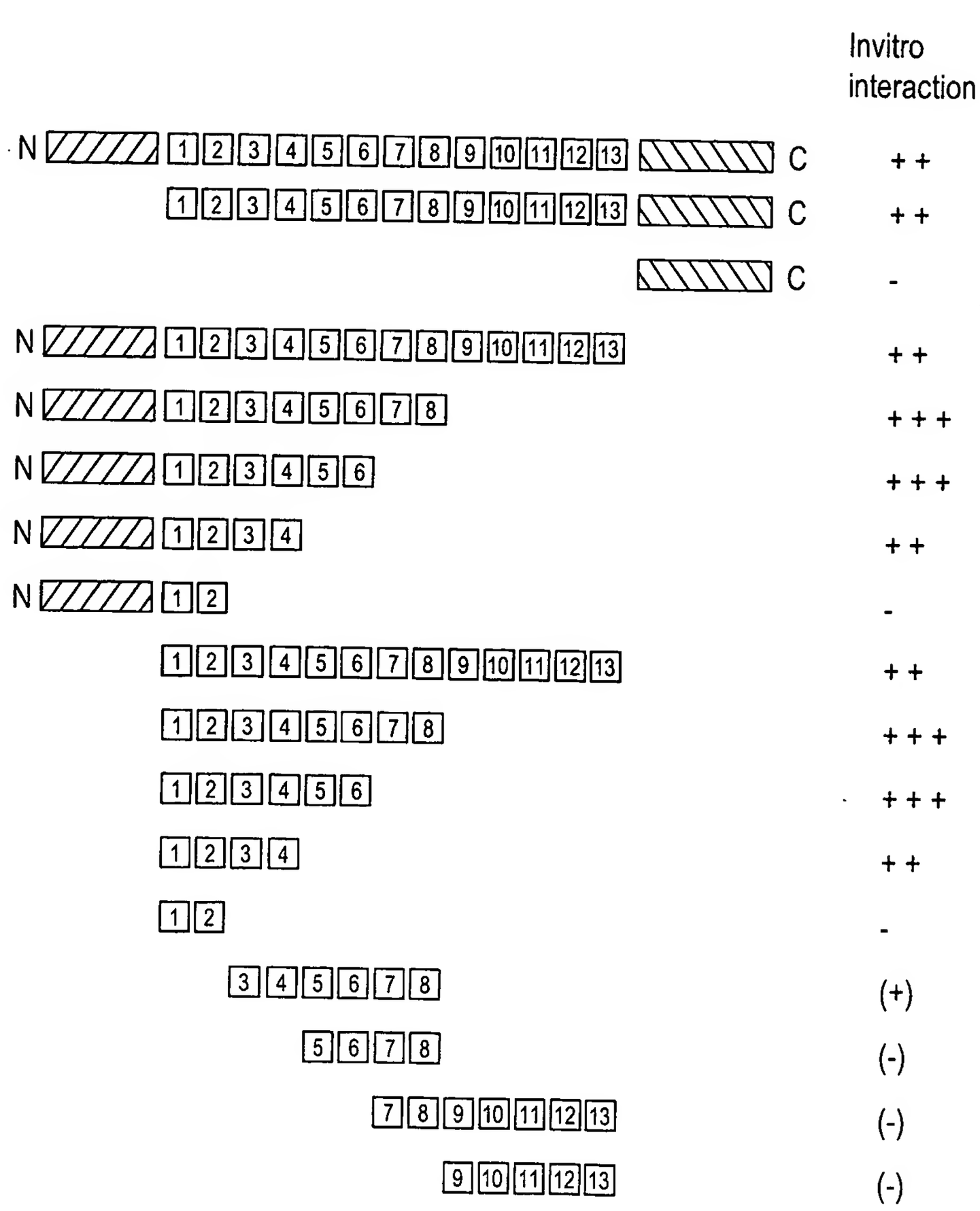
Invitro
interaction
N 1 2 3 4 5 6 7 8 9 10 11 12 13 C ++
1 2 3 4 5 6 7 8 9 10 11 12 13 C ++
C -
N 1 2 3 4 5 6 7 8 9 10 11 12 13 ++
N 1 2 3 4 5 6 7 8 +++
N 1 2 3 4 5 6 +++
N 1 2 3 4 ++
N 1 2 -
1 2 3 4 5 6 7 8 9 10 11 12 13 ++
1 2 3 4 5 6 7 8 +++
1 2 3 4 5 6 +++
1 2 3 4 ++
1 2 -
3 4 5 6 7 8 (+)
5 6 7 8 (-)
7 8 9 10 11 12 13 (-)
9 10 11 12 13 (-)

FIG. 13A

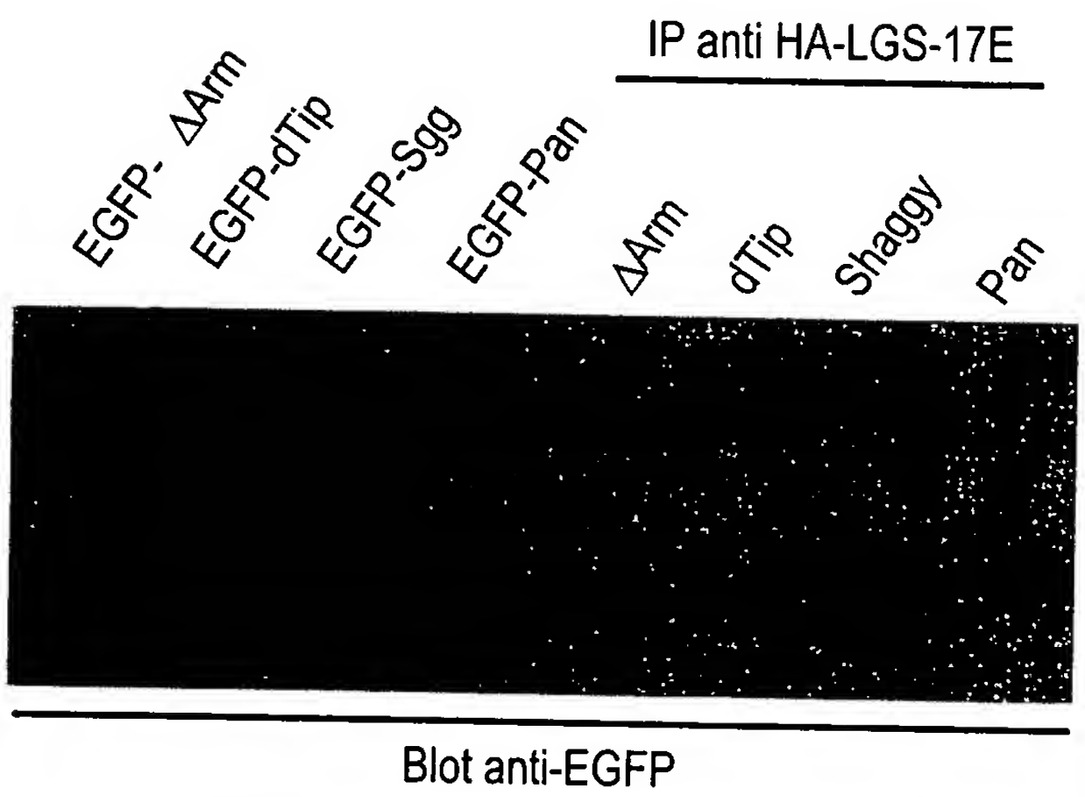

FIG. 13B

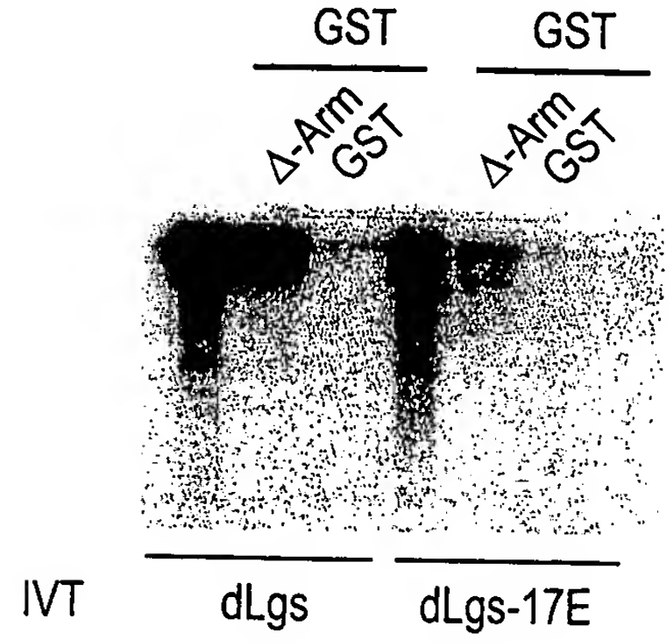

FIG. 13C

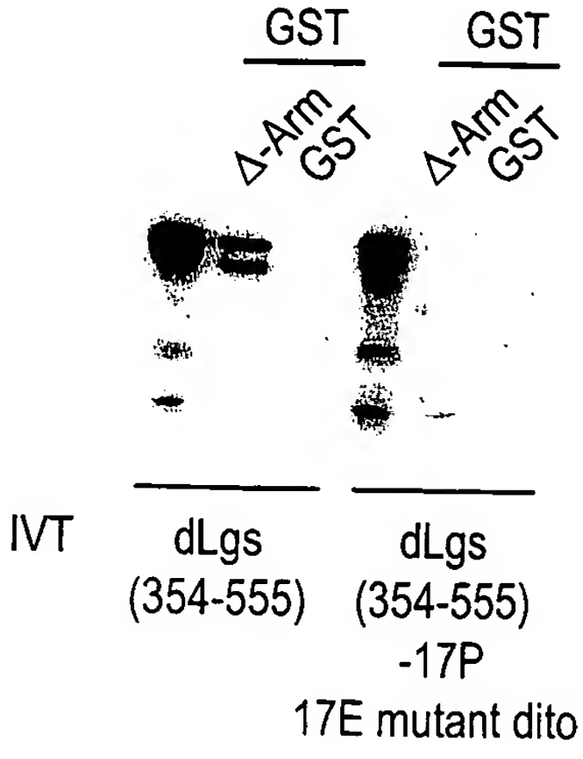

FIG. 13D

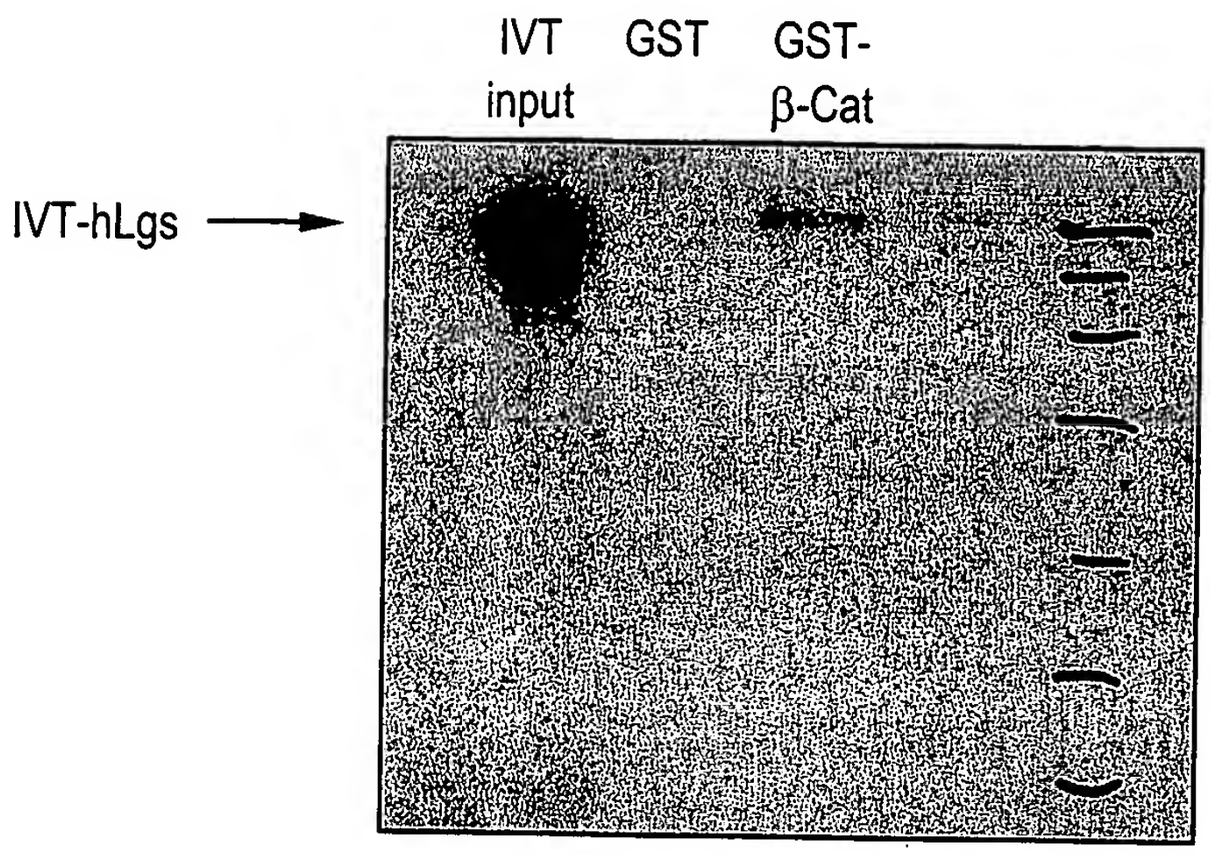

FIG. 13E

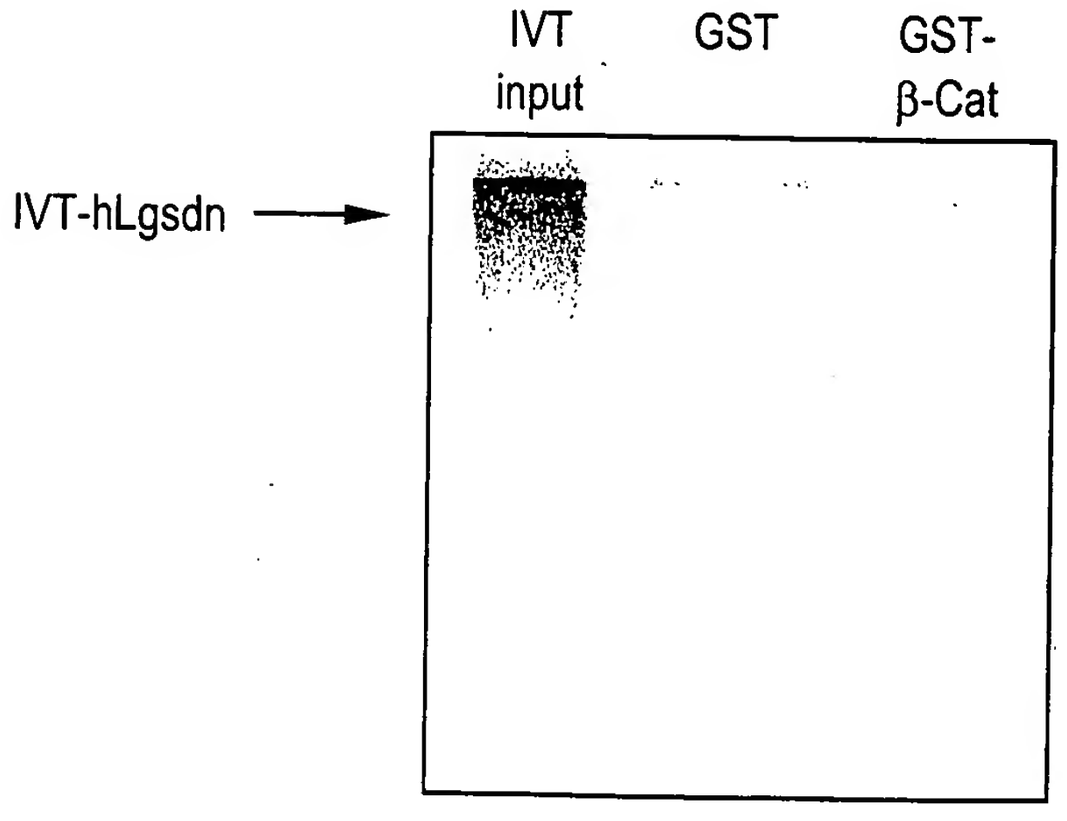

FIG. 14A

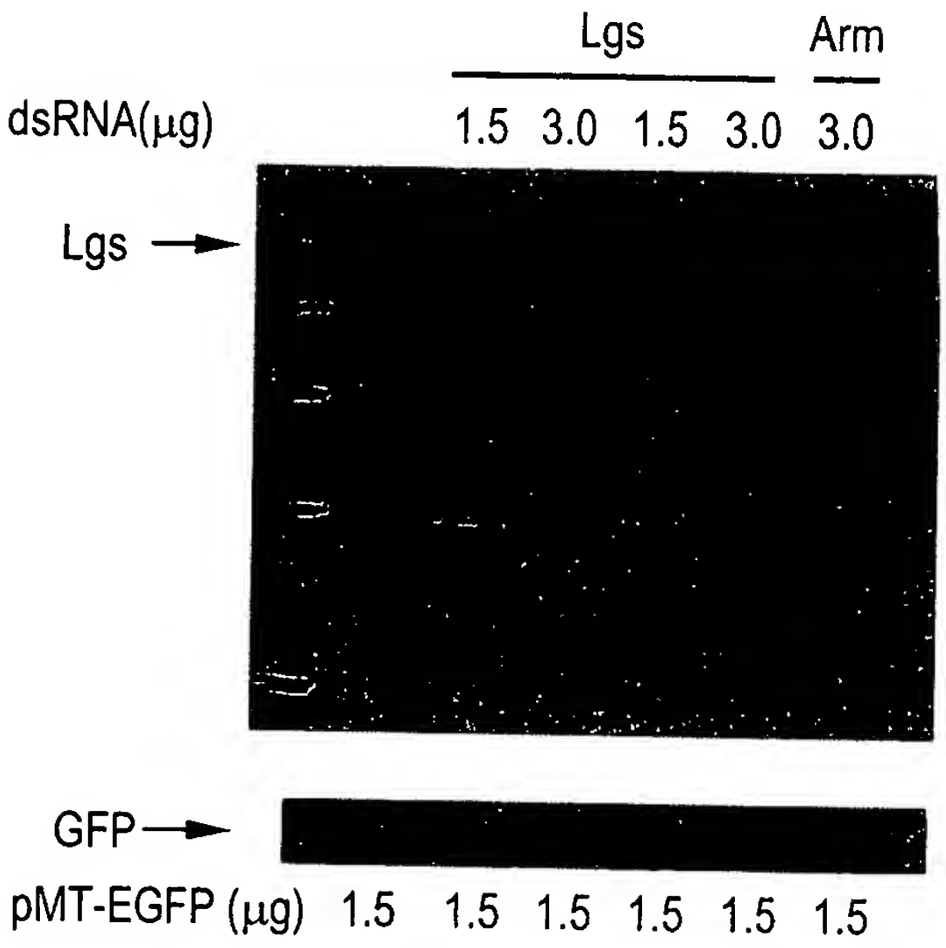

FIG. 14B

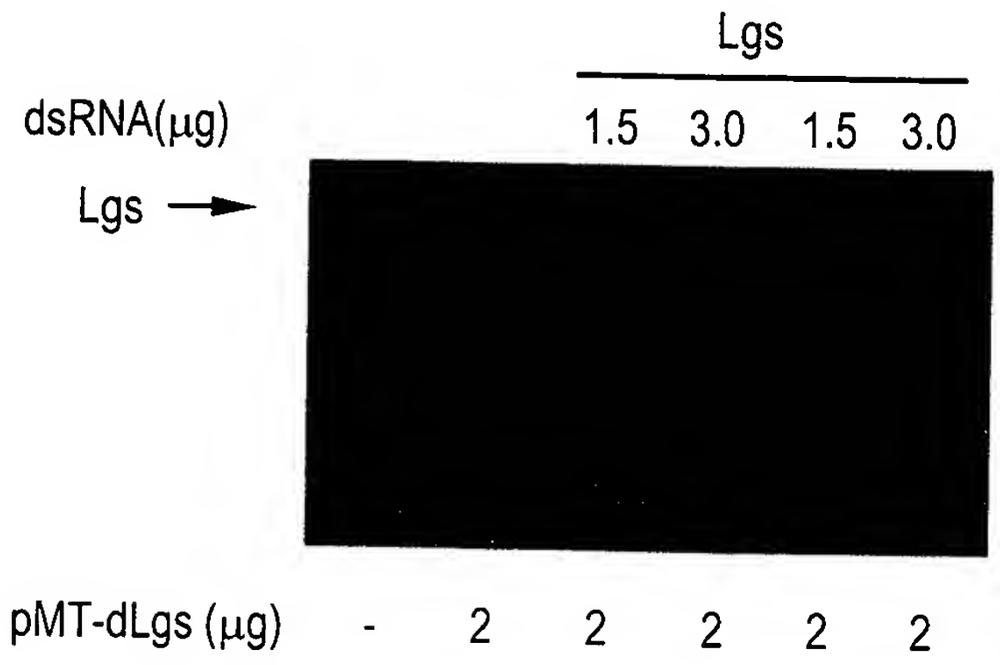

FIG. 15A

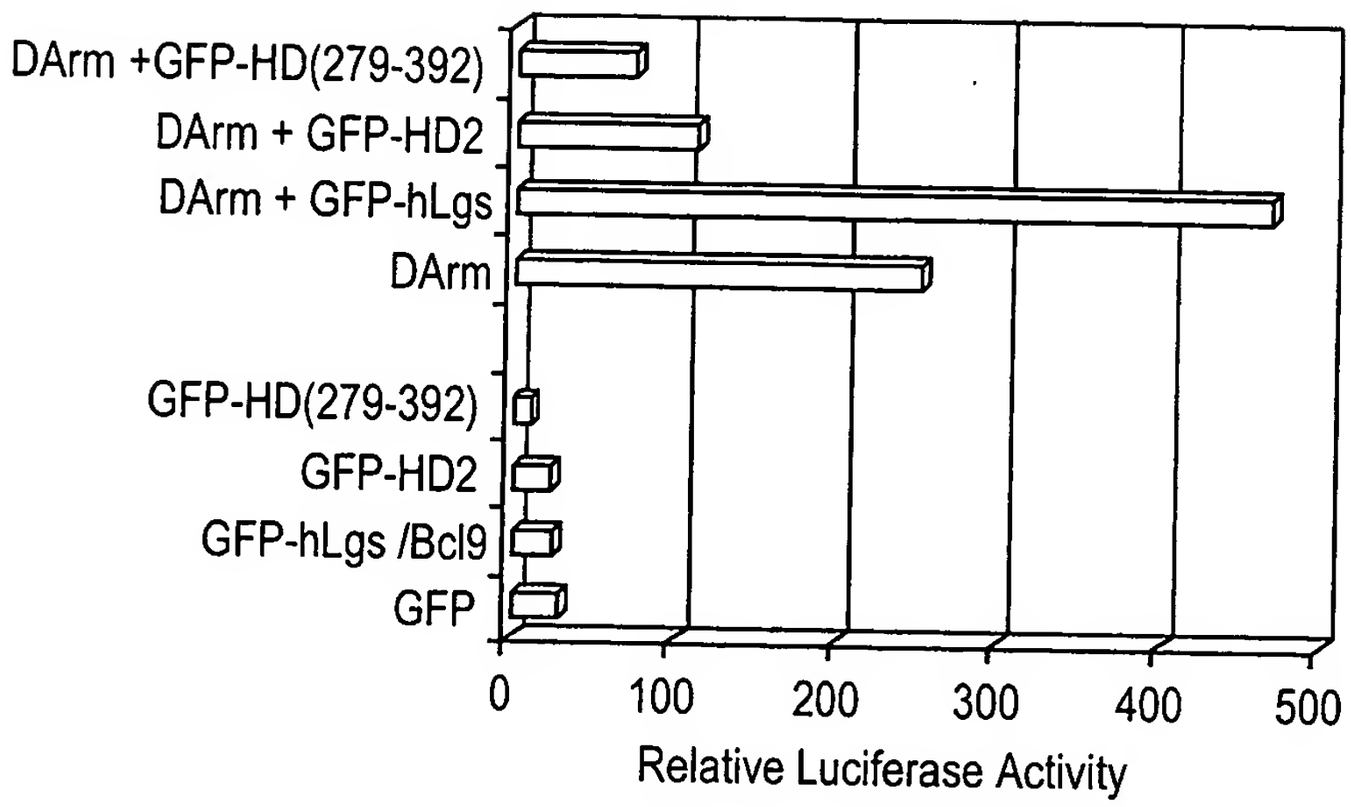

FIG. 15B